



SspI

6358	TCATCAAAATATTAGCAGCATCCAGATTGGGTTCAATCAACAAGGTACGAGCCATATC	6417
	AGTAGTTTTATAAATCGTCGTAGGICTAACCCAAAGTTAGTTGTTCCATGCTCGGTATAG	
6418	ACTTTATTCAAATTGGTATCGCCAAACCAAGAAGAACTCCCATCCTCAAAGGTTTGTA	6477
	TGAAATAAGTTTAACCATAGCGGTTTTGGTTCTTCCTTGAGGTTAGGAGTTTCCAAACAT	
6478	AGGAAGAATTCTCAGTCCAAGCCTCAACAAGGTCAGGGTACAGAGTCTCCAACCATTA	6537
	TCCTTCTTAAGAGTCAGGTTTCGGAGTTGTTCCAGTCCCATGTCTCAGAGGTTTGGTAAT	
6538	GCCAAAAGCTACAGGAGATCAATGAAGAATCTTCAATCAAAGTAACTACTGTTCCAGCA	6597
	CGGTTTTCGATGTCCTCTAGTTACTTCTTAGAAGTTAGTTTTCATTGATGACAAGGTCGT	
6598	CATGCATCATGGTCAGTAAGTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGG	6657
	GTACGTAGTACCAGTCATTCAAAGTCTTTTCTGTAGGTGGCTTCTGAATTTCAATCACC	

FIG. 1A

6658 GCATCTTTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACCAGACAAAAA 6717  
CGTAGAAACTTTTCATTAGAACAGTTGTAGCTCGTCGACCGAACACCCCTGGTCIGTTTTT  
6718 AGGAATGGTGCAGAATTGTTAGGCGCACCTACCAAAGCATCTTTGCCCTTTATTGCAAAG 6777  
TCCTTACCACGTCCTTAACAATCCGCGTGGATGGTTTTCTGTAGAAACGGAAATAACGTTTC  
6838 ATAAAGCAGATTCCCTCTAGTACAAGTGGGGAACAAAAATAACGTGGAAAGAGCTGTCCTG 6897  
TGTCGGGTGAGTGATTTACGCATACTGCTTGGCTCACTGCTGGTGTCTTCTTAAGGGAGAT  
SspI  
6898 TATAAGAAGGCATTCAATCCCATTTGAAGGATCATCAGATACTAACCAATATTTCTC 6954  
ATATTCTCCGTAAGTAAGGTAACCTTCCTAGTAGTCTATGATTGGTTATAAAGAG

FIG. 1B

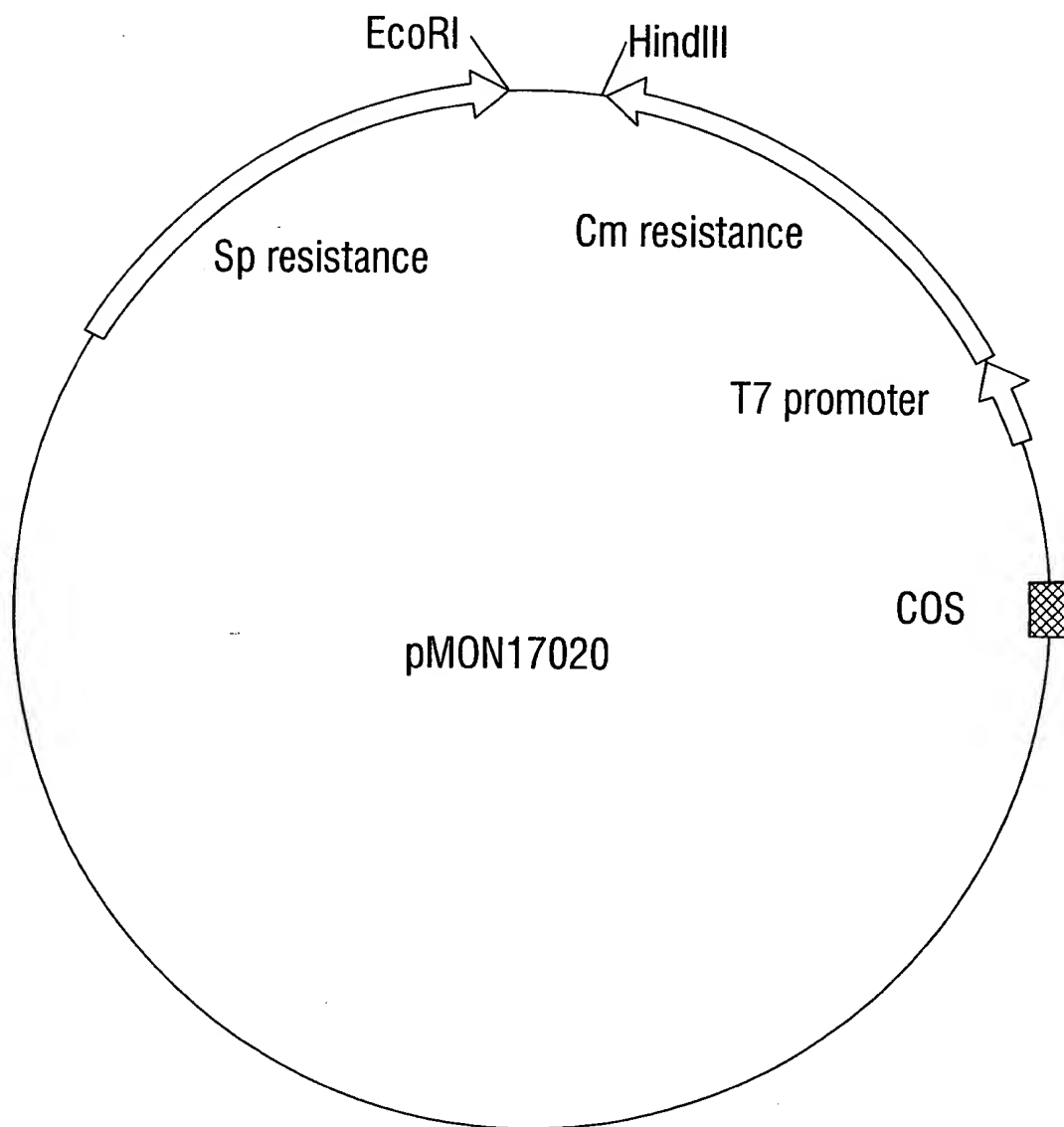


FIG. 2

FIG. 3A

FIG. 3B

CAG GGC TTT GGC GCC AAC CTT ACC GTC GAG ACG GAT GCG GAC GGC GTG Gln Gly Phe 210 Thr Val Glu Thr Asp Ala 220 Gly Val	730
CGC ACC ATC CGC CTG GAA GGC CGC GGC AAG CTC ACC GGC CAA GTC ATC Arg Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile	778
GAC GTG CCG GGC GAC CCG TCC TCG ACG GCC TTC CCG CTG GTT GCG GCC Asp Val Pro Pro Asp 245 Ser Ser Thr Ala Phe 250 Val Ala Ala 255	826
CTG CTT GTT CCG GGC TCC GAC GTC ACC ATC CTC Ile Leu Asn Val Leu Met Asn Leu Leu Val Pro Gly Ser 260 Thr 265	874
CCC ACC CGC ACC GGC CTC ATC CTG ACG CTG CAG GAA ATG GGC GCC GAC Pro Thr Arg Thr Gly 275 Thr Leu 280 Thr Leu Glu Met 285 Gly Ala Asp	922
ATC GAA GTC ATC AAG CCG CGC CTT GCC GGC GGC GAA GAC GTG GCG GAC Ile Glu Val Ile Asn Pro Arg Leu 295 Ala Gly Gly Glu Asp Val Ala Asp	970
CTG CGC GTT CGC TCC TCC ACG CTG AAG GGC GTC ACG GTG CCG GAA GAC Leu Arg Val Arg Ser 310 Thr Leu Lys Gly Val Thr Val Pro Glu Asp	1018

FIG. 3C

CGC GCG CCT TCG ATG ATC GAC GAA TAT CCG ATT CTC GCT GTC GCC GCC	1066
Arg Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala	320 325 330 335
GCC TTC GCG GAA GGG GCG ACC GTG ATG AAC GGT CTG GAA GAA CTC CGC	1114
Ala Phe Ala Glu Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg	340 345 350
GTC AAG GAA AGC GAC CGC CTC TCG GCC GGC AAT GGC CTC AAG CTC	1162
Val Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu	355 360 365
AAT GGC GTG GAT TGC GAT GAG GGC GAG ACG TCG CTC GTC GTG CGC GGC	1210
Asn Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly	370 375 380
CGC CCT GAC GGC AAG GGG CTC GGC AAC GCC TCG GGC GCC GTC GCC	1258
Arg Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala	385 390 395
ACC CAT CTC GAT CAC CGC ATC GCC ATG AGC TTC CTC GTC ATG GGC CTC	1306
Thr His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu	400 405 410 415
GTG TCG GAA AAC CCT GTC ACG GTG GAC GAT GCC ACG ATG ATC GCC ACG	1354
Val Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr	420 425 430

FIG. 3D

AGC TTC CCG GAG TTC ATG GAC CTG ATG GCC GGG CTG GGC GCG AAG ATC	1402
Ser Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile	
435	440
GAA CTC TCC GAT ACG AAG GCT GCC TGATGACCTT CACAATCGCC ATCGATGGTC	1456
Glu Leu Ser Asp Thr Lys Ala Ala	
450	455
CCGCTGCGGC CGGCAAGGGG ACGCTCTCGC GCCGTATCGC GGAGGTCTAT GGCTTTTCATC	1516
ATCTCGATAC GGGCCTGACC TATCGCGCCA CGGCCAAAGC GCTGCTCGAT CGCGGCCCTGT	1576
CGCTTGATGA CGAGGCGGTT GCGGCCGATG TCGCCCGCAA TCTCGATCTT GCCGGGCTCG	1636
ACCGGTCGGT GCTGTCGGCC CATGCCATCG GCGAGGCGGC TTCGAAGATC GCGGTCATGC	1696
CCTCGGTGCG GCGGGCGCTG GTCGAGGCGC AGCGCAGCTT TGCGGCGCGT GAGCCGGGCA	1756
CGGTGCTGGA TGGACGCGAT ATCGGCACGG TGGTCTGCCC GGATGCGCCG GTGAAGCTCT	1816
ATGTCACCGC GTCACCGGAA GTGCGCGCGA AACGCCGCTA TGACGAAATC CTCGGCAATG	1876
GCGGGTTGGC CGATTACGGG ACGATCCTCG AGGATATCCG CCGCCGCGAC GAGCGGGACA	1936
TGGGTCGGGC GGACAGTCCT TTGAAGCCCG CCGACGATGC GCACCTT	1982

FIG. 3E



GTAGCCACAC	ATAATTACTA	TAGTAGGAA	GCCCGCTATC	TCTCAATCCC	GCGTGATCGC	60
GCCAAAATGT	GA CTGTGAAA	AATCC	ATG TCC	CAT TCT	GCA TCC CCG AAA CCA	112
	Met Ser	His Ser	Ala Ser	Pro Lys	Pro	
	1		5			
GCA ACC GCC CGC CGC	TCG GAG GCA CTC	ACG GGC GAA	ATC CGC	ATT CCG		160
Ala Thr Ala Arg Arg	Ser Glu Ala Leu Thr	Gly Glu Ile Arg	Ile Pro			
10	15	20	25			
GGC GAC AAG TCC ATC	TCG CAT CGC TCC	TTC ATG TTT	GGC GGT CTC	GCA		208
Gly Asp Lys Ser Ile Ser	His Arg Ser Phe	Met Phe Gly Gly	Leu Ala			
	30	35	40			
TCG GGC GAA ACC CGC	ATC ACC GGC CTT	CTG GAA GGC	GAG GAC GTC	ATC		256
Ser Gly Glu Thr Arg	Ile Thr Gly Leu	Glu Leu Gly Asp	Val Ile			
45	50	55				
AAT ACA GGC CGC GCC	ATG CAG GCC ATG	GGC GCG AAA	ATC CGT AAA	GAG		304
Asn Thr Gly Arg Ala	Met Gln Ala Met	Gly Ala Lys Ile	Arg Lys Glu			
60	65	70				
GGC GAT GTC TGG ATC	AAC GGC GTC	GGC AAT GGC	TGC CTG	TTG CAG		352
Gly Asp Val Trp	Ile Ile Asn Gly	Val Gly Asn Gly	Cys Leu	Gln		
75	80	85				

FIG. 4A

CCC GAA GCT GCG CTC GAT TTC GGC AAT GCC GGA ACC GGC GCG CTC	400
Pro Glu Ala Ala Ser Leu 95	
90	
ACC ATG GGC CTT GTC GGC ACC TAT GAC ATG AAG ACC TCC TTT ATC GGC	448
Thr Met Gly Leu Val 110	
115	
GAC GCC TCG CTG TCG AAG CCG CCG ATG GGC CGC GTG CTG AAC CCG TTG	496
Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu 135	
130	
CGC GAA ATG GGC GTT CAG GTG GAA GCA GCC GAT GGC GAC CGC ATG CCG	544
Arg Glu Met Gly Val Gln Val 145	
140	
CTG ACG CTG ATC GGC CCG AAG ACG GCC AAT CCG ATC ACC TAT CGC GTG	592
Leu Thr Leu Ile Gly Pro Lys 160	
155	
CCG ATG GCC TCC GCG CAG GTA AAA TCC GCC GTG CTG CTC GGT CTC	640
Pro Met Ala Ser Ala Gln Val 175	
170	
AAC ACG CCG GGC GTC ACC ACC GTC ATC GAG CCG GTC ATG ACC CGC GAC	688
Asn Thr Pro Gly Val Thr 190	
195	
200	

FIG. 4B

CAC ACC GAA AAG ATG CTG CAG GGC TTT GGC GCC GAC CTC ACG GTC GAG His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr Val Glu	205 210 215	736
ACC GAC AAG GAT GGC GTG CGC CAT ATC CGC ATC ACC GGC CAG GGC AAG Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln Gly Lys	220 225	784
CTT GTC GGC CAG ACC ATC GAC GTG CCG GGC GAT CCG TCA TCG ACC GCC Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser Thr Ala	235 240 245	832
TTC CCG CTC GTT GCC GCC GAT CTT CTG GTG GAA GGT TCC GAC GTC ACC ATC Phe Pro Leu Val Ala Ala Leu Leu Val Glu Gly Ser Asp Val Thr Ile	250 255 260	880
CGC AAC GTG CTG ATG AAC CCG ACC CGT ACC GGC CTC ATC CTC ACC TTG Arg Asn Val Leu Met Met Asn Pro Thr Arg Thr Gly Leu Ile Leu Thr Leu	270 275	928
CAG GAA ATG GGC GCC GAT ATC GAA GTG CTC AAT GCC CGT CTT GCA GGC Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu Ala Gly	285 290	976
GGC GAA GAC GTC GCC GAT CTG CGC GTC AGG GCT TCG AAG CTC AAG GGC Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu Lys Gly	300 305 310	1024

FIG. 4C

GTC Val 315	GTC Val 315	GTT Val 315	CCG Pro 315	CCG Pro 315	CCG Pro 315	GAA Glu 315	CGT Arg 320	GCG Ala 320	TCG Ser 325	ATG Met 325	ATC Ile 325	GAC Asp 325	GAA Glu 325	TAT Tyr 325	CCG Pro 325	1072
GTC Val 330	CTG Leu 330	GCG Ala 330	ATT Ile 330	GCC Ala 335	GCC Ala 335	TCC Ser 335	TTC Phe 340	GCG Ala 340	GAA Glu 340	GGC Gly 340	GAA Glu 340	ACC Thr 340	GTG Val 340	ATG Met 340	GAC Asp 345	1120
GGG Gly 350	CTC Leu 350	GAC Asp 350	GAA Glu 350	CTG Leu 350	CGC Arg 350	GTC Val 350	AAG Lys 355	GAA Glu 355	TCG Ser 355	GAT Asp 355	CGT Arg 355	CTG Leu 360	GCA Ala 360	GCG Glu 360	GTC Val 360	1168
GCA Ala 365	CGC Arg 365	GGC Gly 365	CTT Leu 365	GAA Glu 370	GCC Ala 370	AAC Asn 370	GGC Gly 370	GTC Val 370	GAT Asp 375	TGC Cys 375	ACC Thr 375	GAA Glu 375	GGC Gly 375	GAG Glu 375	ATG Met 375	1216
TCG Ser 380	CTG Leu 380	ACG Thr 380	GTT Val 380	CGC Arg 385	GGC Gly 385	CGC Arg 385	CCC Pro 385	GAC Asp 385	GGC Gly 390	AAG Lys 390	GGA Gly 390	CTG Leu 390	GGC Gly 390	GGC Gly 390	GGC Gly 390	1264
ACG Thr 395	GTT Val 395	GCA Ala 395	ACC Thr 395	CAT His 400	CTC Leu 400	GAT Asp 400	CAT His 400	CGT Arg 405	ATC Ile 405	GCG Ala 405	ATG Met 405	AGC Ser 405	TTC Phe 405	CTC Leu 405	GTG Val 405	1312
ATG Met 410	GGC Gly 410	CTT Leu 410	GCG Ala 415	GAA Glu 415	AAG Lys 415	CCG Pro 420	GTG Val 420	ACG Thr 420	GTT Val 420	GAC Asp 420	GAC Asp 420	AGT Ser 425	AAC Asn 425	ATG Met 425	ATG Met 425	1360

FIG. 4D

ATC GCC ACG TCC TTC CCC GAA TTC ATG GAC ATG ATG CCG GGA TTG GGC Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Met Met Pro Gly Leu Gly 430 435 440	1408
GCA AAG ATC GAG TTG AGC ATA CTC TAGTCACTCG ACAGCGAAAA TATTATTTC Ala Lys Ile Glu Leu Ser Ile Leu 445	1462
GAGATTGGGC ATTATTACCG GTTGGTCTCA GCGGGGGTTT AATGTCCAAT CTTCATACG TAACAGCATC AGGAAATATC AAAAAAGCTT TAGAAGGAAT TGCTAGAGCA GCGACGCCGC CTAAGCTTTC TCAAGACTTC GTTAAAACTG TACTGAAATC CCGGGGGGTC CGGGGATCAA ATGACTTCAT TTCTGAGAAA TTGGCCTCGC A	1522 1582 1642 1673

FIG. 4E

GTGATCGCGC CAAATGTGA CTGTGAAAAA TCC ATG TCC CAT TCT GCA TCC CCG	54
Met Ser His Ser Ala Ser Pro	5
AAA CCA GCA ACC GCC CGC CGC TCG GAG GCA CTC ACG GGC GAA ATC CGC	102
Lys Pro Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg	20
ATT CCG GGC GAC AAG TCC ATC TCG CAT CGC TCC TTC ATG TTT GGC GGT	150
Ile Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly	35
CTC GCA TCG GGC GAA ACC CGC ATC ACC GGC CTT CTG GAA GGC GAG GAC	198
Leu Ala Ser Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp	55
GTC ATC AAT ACA GGC CGC GCC ATG CAG GCC ATG GGC GCG AAA ATC CGT	246
Val Ile Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg	70
AAA GAG GGC GAT GTC TGG ATC ATC AAC GGC GTC GGC AAT GGC TGC CTG	294
Lys Glu Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu	85
TTG CAG CCC GAA GCT GCG CTC GAT TTC GGC AAT GCC GGA ACC GGC GCG	342
Leu Gln Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala	100

FIG. 5A

CGC CTC ACC ATG GGC CTT GTC GGC ACC TAT GAC ATG AAG ACC TCC TTT	390
Arg Leu 105 Thr Met Gly Leu 110 Val Gly Thr Asp Met 115 Lys Thr Ser Phe	
ATC GGC GAC GCC TCG CTG TCG AAG CGC CGC ATG GGC CGC GTG CTG AAC	438
Ile Gly 120 Asp Ala Ser Leu 125 Ser Leu Arg Lys Arg Met 130 Gly Val Leu Asn 135	
CCG TTG CGC GAA ATG GGC GTT CAG GTG GAA GCA GCC GAT GGC GAC CGC	486
Pro Leu Arg Glu Met 140 Val Gln Val Glu Ala Ala Asp Gly Asp Arg 150	
ATG CCG CTG ACG CTG ATC GGC CCG AAG ACG GCC AAT CCG ATC ACC TAT	534
Met Pro Leu 155 Thr Leu Ile Gly Pro 160 Lys Thr Ala Asn Pro Ile Thr Tyr 165	
CGC GTG CCG ATG GCC TCC GCG CAG GTA AAA TCC GCC GTG CTG CTC GCC	582
Arg Val 170 Pro Met Ala Ser Ala 175 Gln Val Lys Ser Ala Val Leu Ala 180	
GGT CTC AAC ACG CCG GGC GTC ACC ACC GTC ATC GAG CCG GTC ATG ACC	630
Gly Leu 185 Asn Thr Pro Gly Val 190 Thr Thr Val Ile Glu 195 Pro Val Met Thr 200	
CGC GAC CAC ACC GAA AAG ATG CTG CAG GGC TTT GGC GCC GAC CTC ACG	678
Arg Asp 200 His Thr Glu Lys Met Leu Gln Gly Phe 210 Gly Ala Asp Leu 215	

FIG. 5B

GTC GAG ACC GAC AAG GAT GGC GTG CGC CAT ATC CGC ATC ACC GGC CAG Val Glu Thr Asp Lys Asp 220 225	726
GGC AAG CTT GTC GGC CAG ACC ATC GAC GTG CCG GGC GAT CCG TCA TCG Gly Lys Leu Val 235 240	774
ACC GCC TTC CCG CTC GTT GCC GCC ATG AAC CCG CTT CTG GTG GAA GGT TCC GAC GTC Thr Ala Phe Pro Leu Val 250 255	822
ACC ATC CGC AAC GTG CTG ATG AAC CCG ACC CGT ACC GGC CTC ATC CTC Thr Ile Arg Asn Val 265 270	870
ACC TTG CAG GAA ATG GGC GCC GAT ATC GAA GTG CTC AAT GCC CGT CTT Thr Leu Glu Met 285 290	918
GCA GGC GGC GAA GAC GTC GTC GCC GAT CTG CGC GTC AGG GCT TCG AAG CTC Ala Gly Gly Glu Asp 300 305	966
AAG GGC GTC GTC GTT CCG CCG GAA CGT GCG CCG CTG ATG ATC GAC GAA Lys Gly Val Val 315 320	1014

FIG. 5C



TAT CCG GTC CTG GCG ATT GCC GCC TTC TCC TCC TTC GCG GAA GGC GAA ACC GTG Tyr Pro Val 330 Leu Ala Ile Ala Ala Ser Phe Ala Glu Gly Thr Val 340	1062
ATG GAC GGG CTC GAC GAA GAA CTG CGC GTC AAG GAA TCG GAT CGT CTG GCA Met Asp 345 Gly Leu Asp Glu 350 Leu Arg Val Lys Glu Ser Asp Arg Leu Ala 355	1110
GCG GTC GCA CGC GGC CTT GAA GCC AAC GGC GTC GAT TGC ACC GAA GGC Ala Val Ala Arg Gly Leu 365 Glu Ala Asn Gly Val Asp Cys Thr Glu Gly 375	1158
GAG ATG TCG CTG ACG GTT CGC GGC CGC CCC GAC GGC AAG GGA CTG GGC Glu Met Ser Leu Thr Val 380 Thr Val Arg Gly Arg Pro 385 Asp Gly Lys Gly Leu Gly 390	1206
GGC GGC ACG GTT GCA ACC CAT CTC GAT CAT CAT CGT ATC GCG ATG AGC TTC Gly Gly Thr Val 395 Val Ala Thr His Leu Asp 400 His Arg Ile Ala Met Ser Phe 405	1254
CTC GTG ATG GGC CTT GCG GCG GAA AAG AAG CCG GTG ACG GTT GAC GAC AGT Leu Val Met Gly Leu Ala Ala Glu 415 Lys Pro Pro Val Thr Val Asp Asp Ser 420	1302
AAC ATG ATC GCC ACG TCC TTC CCC GAA TTC ATG GAC ATG ATG CCG GGA Asn Met Ile Ala Thr Ser 430 Phe Pro Glu Phe Met Met Met Pro Gly 435	1350

FIG. 5D

TTG GGC GCA AAG ATC GAG TTG AGC ATA CTC TAGTCACTCG ACAGCGAAAA	1400
Leu Gly Ala Lys Ile Glu Leu Ser Ile Leu	
440	
445	
TATTATTTCG GAGATTGGGC ATTATTACCG GTTGGTCTCA GCGGGGGTTT AATGTCCAAT	1460
CTTCCATACG TAACAGCATC AGGAAATATC AAAAAAGCTT	1500

FIG. 5E

1 MSHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGL 50  
1 .....MESLTLOPIARVDGTINLPGSKTVSNRALLLAALAHGKTVLTNL 44  
51 LEGEDVINTGKAMQAMGARIRKEGDTWIIDGVGNGGGLLAPEAPLD..FGN 98  
45 LDSDDVRHMLNAL TALGVSYTL SADRTRCEIIGNGGPLHAEGALELFLGN 94  
99 AATGCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVK.SÉ 147  
95 AGTAMRPLAAALCLGSNDIVLTGEPRMKERPIGHLVDALRLGGAKITYLE 144  
148 DGDRLPVTLRGPKTPTPIITYRVPMAQAQKSAVLLAGLNTPGITTVEPI 197  
145 QENYPPLRLQGGFTGGNVDDVDSVSSQFLTALLMTAPLAPEDTVIRIKGD 194  
198 MTRDHTKMLQGFGANLTVÉTDADGVRTIRLEGRGKLTGQVIDVPGDPSS 247  
195 LVSKPYIDITLNL MKTFGVEIENQHYYQQFVVKGGQSYQSPGTYLVEGDAS 244

FIG. 6A

248 TAFPLVAALLVPGSDVTILNVLMNPTRTGLILT..LQEMGADIEVINPRL 295  
245 SASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATI..... 287  
296 AGGEDVADLRVRSSTLKGVTVPEDRAPSMIDEYPILAVAAFAEGATVMN 345  
288 CWGDDY..ISCTRGELNAIDMDMINHIP...DAAMTIATAALFAKGTTRLR 332  
346 GLEELRVKESDRLSAVANGKLNGVDCDEGETSLVWRGPDGKGLGNASG 395  
333 NIYNWRVKETDRLFAMATELRKVGAEEVEEGHDYIRI.TPPEKLN..... 376  
396 AAVATHLDHRIAMSFLVMGLVSENPTVDDATMIATSFPEFMDLMAGLGA 445  
377 AEIATYNDHRMAMCFSLVAL.SDTPVTILDPKCTAKTFPDYFEQLARISQ 425  
446 KIELSDTKAA\* 456  
426 AA\* ..... 428

FIG. 6B

FIG. 7A



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CCATGGCTCA CCGTGCAAGC AGCCGTCCAG CAACTGCTCG TAAGTCCTCT GGTCTTTCTG   60
GAACCGTCCG TATTCAGGT GACAAGTCTA TCTCCACAG GTCCTTCATG TTTGGAGGTC   120
TCGCTAGCGG TGAAACTCGT ATCACCGGTC TTTTGGGAAGG TGAAGATGTT ATCAACACTG   180
GTAAGGCTAT GCAAGCTATG GGTGCCAGAA TCCGTAAGGA AGGTGATACT TGGATCATTG   240
ATGGTGTGG TAACGGTGA CTCCTTGC TCAGGGCTCC TCICGATTTC GGTAAACGCTG   300
CAACTGGTTG CCGTTTGACT ATGGTCTTG TTGGTGTTTA CGATTTTCGAT AGCACTTTCA   360
TTGGTGACGC TTCCTCACT AAGCGTCCAA TGGGTCGTGT GTTGAACCCA CTTGCGGAAA   420
TGGGTGTGCA GGTGAAGTCT GAAGACGGTG ATCGTCTTCC AGTTACCTTG CGTGGACCAA   480
AGACTCCAAC GCCAATCACC TACAGGGTAC CTATGGCTTC CGCTCAAGTG AAGTCCGCTG   540
TTCGTCTTGC TGGTCTCAAC ACCCCAGGTA TCACCACTGT TATCGAGCCA ATCATGACTC   600
GTGACCACAC TGAAAAGATG CTTCAAGTT TTGGTGCTAA CCTTACCGTT GAGACTGATG   660
CTGACGGTGT GCGTACCATC CGTCTTGAAG GTCGTGGTAA GCTCACC GGTTCAAGTGATTG   720
ATGTTCCAGG TGATCCCTCC TCTACTGCTT TCCCATTTGGT TGCTGCCTTG CTTGTTCCAG   780
GTTCCGACGT CACCATCCTT AACGTTTTGA TGAACCCAAC CCGTACTGGT CTCATCTTGA   840

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FIG. 8A

CTCTGCAGGA AATGGGTGCC GACATCGAAG TGATCAACCC ACGTCTTGCT GGTGGAGAAG 900  
ACGTGGCTGA CTTGCGTGTT CGTTCTTCTA CTTTGAAGGG TGTTACTGTT CCAGAAGACC 960  
GTGCTCCTTC TATGATCGAC GAGTATCCAA TTCTCGCTGT TGCAGCTGCA TTCGCTGAAG 1020  
GTGCTACCGT TATGAACGGT TTGGAAGAAC TCCGIGTTAA GGAAAGCGAC CGTCTTTCTG 1080  
CTGTGCGCAA CGGTCTCAAG CTC AACGGTG TTGATTGCCA TGAAGGTGAG ACTTCTCTCG 1140  
TCGTGCGTGG TCGTCCTGAC GGTAAGGGTC TCGGTAAACGC TTCTGGAGCA GCTGTCGCTA 1200  
CCCACCTCGA TCACCGTATC GCTATGAGCT TCCTCGTTAT GGGTCTCGTT TCTGAAAACC 1260  
CTGTTACTGT TGATGATGCT ACTATGATCG CTA TAGCTT CCCAGAGTTC ATGGATTGTA 1320  
TGGCTGGTCT TGGAGCTAAG ATCGAACTCT CCGACACTAA GGCTGCTTGA TGAGCTC 1377

FIG. 8B



```
CTCTGCAGGA AATGGGTGCC GACATCGAAG TGATCAACCC ACGTCTTGCT GGTGGAGAAG 900
ACGTGGCTGA CTTGCGTGTT CGTTCTTCTA CTTTGAAGGG TGTTACTGTT CCAGAAGACC 960
GTGCTCCTTC TATGATCGAC GAGTATCCAA TTCTCGCTGT TGCAGCTGCA TTCGCTGAAG 1020
GTGCTACCGT TATGAACGGT TTGGAAGAAC TCCGTGTTAA GGAAAGCGAC CGTCTTTCTG 1080
CTGTGCGCAA CGGTCTCAAG CTCACGGTG TTGATTGCCA TGAAGGTGAG ACTTCTCTCG 1140
TCGTGCGTGG TCGTCCTGAC GGTAAAGGTC TCGGTAACGC TTCITGGAGCA GCTGTCGCTA 1200
CCCACCTCGA TCACCGTATC GCTATGAGCT TCCTCGTTAT GGGTCTCGTT TCTGAAAACC 1260
CTGTTACTGT TGATGATGCT ACTATGATCG CTA TAGCTT CCCAGAGTTC ATGGATTGTA 1320
TGGCTGGTCT TGGAGCTAAG ATCGAACTCT CCGACACTAA GGCTGCTTGA TGAGCTC 1377
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FIG. 9

AGATCTATCG	ATAAGCTTGA	TGTAATTGGA	GGAAGATCCA	AATTTTCAAT	CCCCATTCTT	60
CGATTGCTTC	AATTGAAGTT	TCTCCG	ATG GCG CAA	GTT AGC AGA	ATC TGC AAT	113
	Met	Ala	Gln	Val	Ser Arg Ile Cys Asn	
	1				5	
GGT GTG CAG AAC CCA	TCT CTT ATC	TCC AAT	CTC TCG AAA	TCC AGT CAA		161
Gly Val Gln Asn Pro	Ser Leu Ile Ser	Asn Leu Ser	Lys Ser Ser	Gln	25	
	10					
CGC AAA TCT CCC	TTA TCG GTT	TCT CTG AAG	ACG CAG CAT	CCA CGA		209
Arg Lys Ser Pro	Leu Ser Val	Ser Leu Lys	Thr Gln Gln	His Pro Arg	40	
	30					
GCT TAT CCG ATT	TCG TCG TCG	TGG GGA	TTG AAG AAG	AGT GGG	ATG ACG	257
Ala Tyr Pro Ile	Pro Ser Ser	Trp Gly	Leu Lys Ser	Gly Met Thr	55	
	45					

FIG. 10A

TTA ATT GGC TCT GAG CTT CGT CCT CTT AAG GTC ATG TCT TCT GTT TCC	305
Leu Ile Gly Ser Glu Leu Arg Pro Leu Lys Val Met Ser Val Ser	
	70
ACG GCG GAG AAA GCG TCG GAG ATT GTA CTT CAA CCC ATT AGA GAA ATC	353
Thr Ala Glu Lys Ala Ser Glu Ile Val Leu Gln Pro Ile Arg Glu Ile	
	80
	85
TCC GGT CTT ATT AAG TTG CCT GGC TCC AAG TCT CTA TCA AAT AGA ATT	401
Ser Gly Leu Ile Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile	
	90
	95
	100
	105
C	402

FIG. 10B

AGATCTTTCA	AGA	ATG	GCA	CAA	ATT	AAC	AAC	ATG	GCT	CAA	GGG	ATA	CAA	49
		Met	Ala	Gln	Ile	Asn	Asn	Met	Ala	Gln	Gly	Ile	Gln	
		1				5					10			
ACC CTT AAT CCC AAT TCC AAT TTC CAT AAA CCC CAA GTT CCT AAA TCT														97
Thr Leu Asn Pro Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser														
		15				20					25			
TCA AGT TTT CTT GTT TTT GGA TCT AAA AAA CTG AAA AAT TCA GCA AAT														145
Ser Ser Phe Leu Val Phe Gly Ser Lys Lys Lys Leu Lys Asn Ser Ala Asn														
		30				35					40			
TCT ATG TTG GTT TTG AAA AAA GAT TCA ATT TTT ATG CAA AAG TTT TGT														193
Ser Met Leu Val Leu Lys Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys														
		45				50					55			60
TCC TTT AGG ATT TCA GCA TCA GTG GCT ACA GCC TGC ATG C														233
Ser Phe Arg Ile Ser Ala Ser Val Ala Thr Ala Cys Met														
						65					70			

FIG. 11

AGATCTGCTA	GAAATAATTT	TGTTTAACTT	TAAGAAGGAG	ATATATCC	ATG GCA CAA	57
					Met Ala Gln	
					1	
ATT AAC AAC	ATG GCT CAA	GGG ATA CAA	ACC CTT AAT	CCC AAT TCC	AAT	105
Ile Asn Asn	Met Ala Gln	Ile Gln Thr	Leu Asn	Pro Asn Ser	Asn	
5	10	15				
TTC CAT AAA	CCC CAA GTT	CCT AAA TCT	TCA AGT TTT	CTT GTT TTT	GGA	153
Phe His Lys	Pro Gln Val	Pro Lys Ser	Ser Ser Phe	Leu Val Phe	Gly	
20	25	30			35	
TCT AAA AAA	CTG AAA AAT	TCA GCA AAT	TCT ATG TTG	GTT TTT	AAA AAA	201
Ser Lys Lys	Leu Lys Asn	Ala Asn Ser	Met Met Leu	Val Leu Lys	Lys	
	40	45			50	

FIG. 12A

GAT TCA ATT TTT ATG CAA AAG TTT TGT TCC TTT AGG ATT TCA GCA TCA	249
Asp Ser Ile Phe 55 Met Cys Ser Phe Arg Ile Ser Ala Ser	
	60
	65
GTG GCT ACA GCA CAG AAG CCT TCT GAG ATA GTG TTG CAA CCC ATT AAA	297
Val Ala Thr 70 Ala Gln Lys Pro Ser Glu Ile Val Leu Gln Pro Ile Lys	
	75
	80
GAG ATT TCA GGC ACT GTT AAA TTG CCT GGC TCT AAA TCA TTA TCT AAT	345
Glu Ile Ser 85 Gly Thr Val Lys 90 Pro Gly Ser Lys Ser Leu Ser Asn	
	95
AGA ATT C	352
Arg Ile	
100	

FIG. 12B

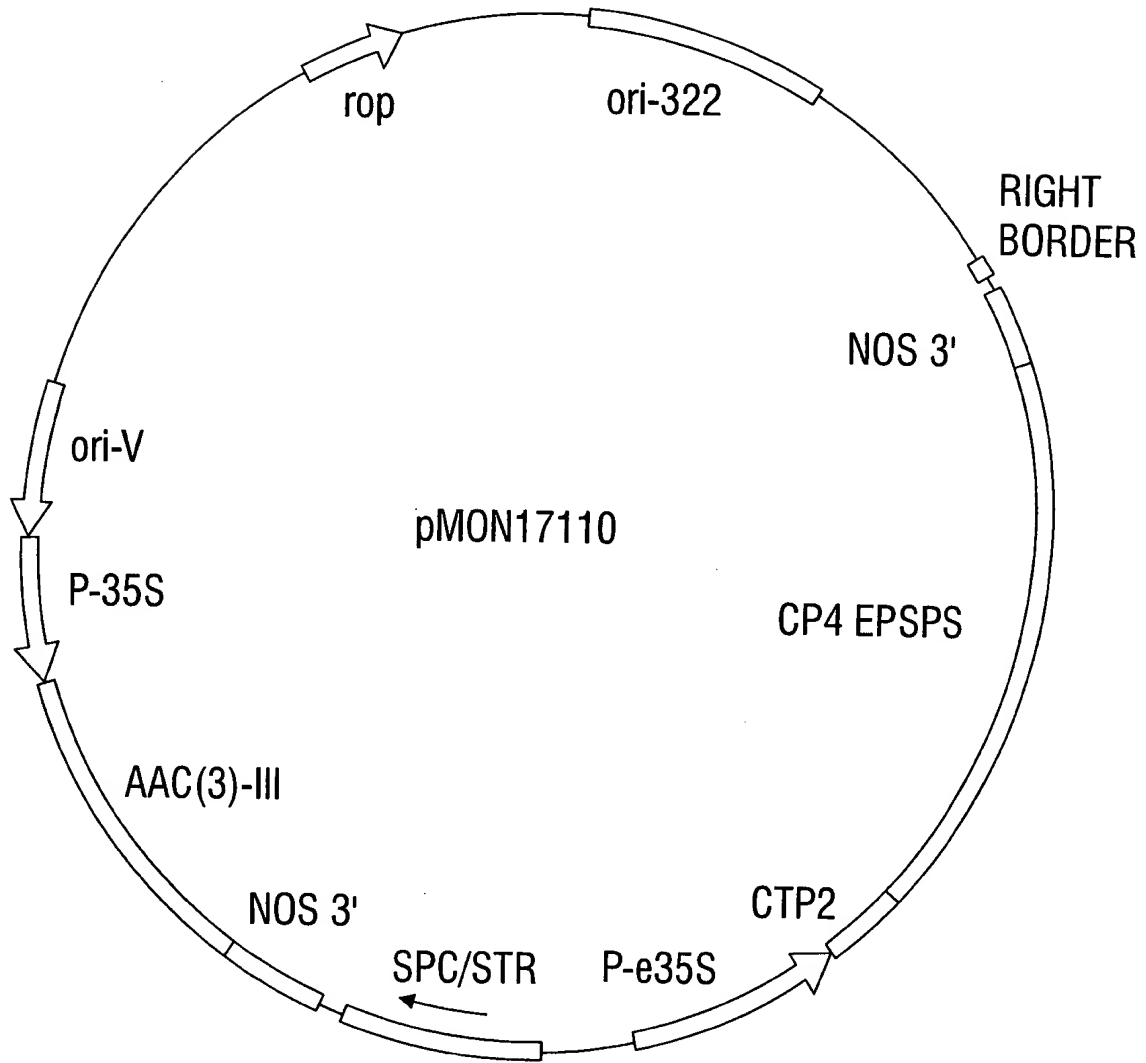


FIG. 13

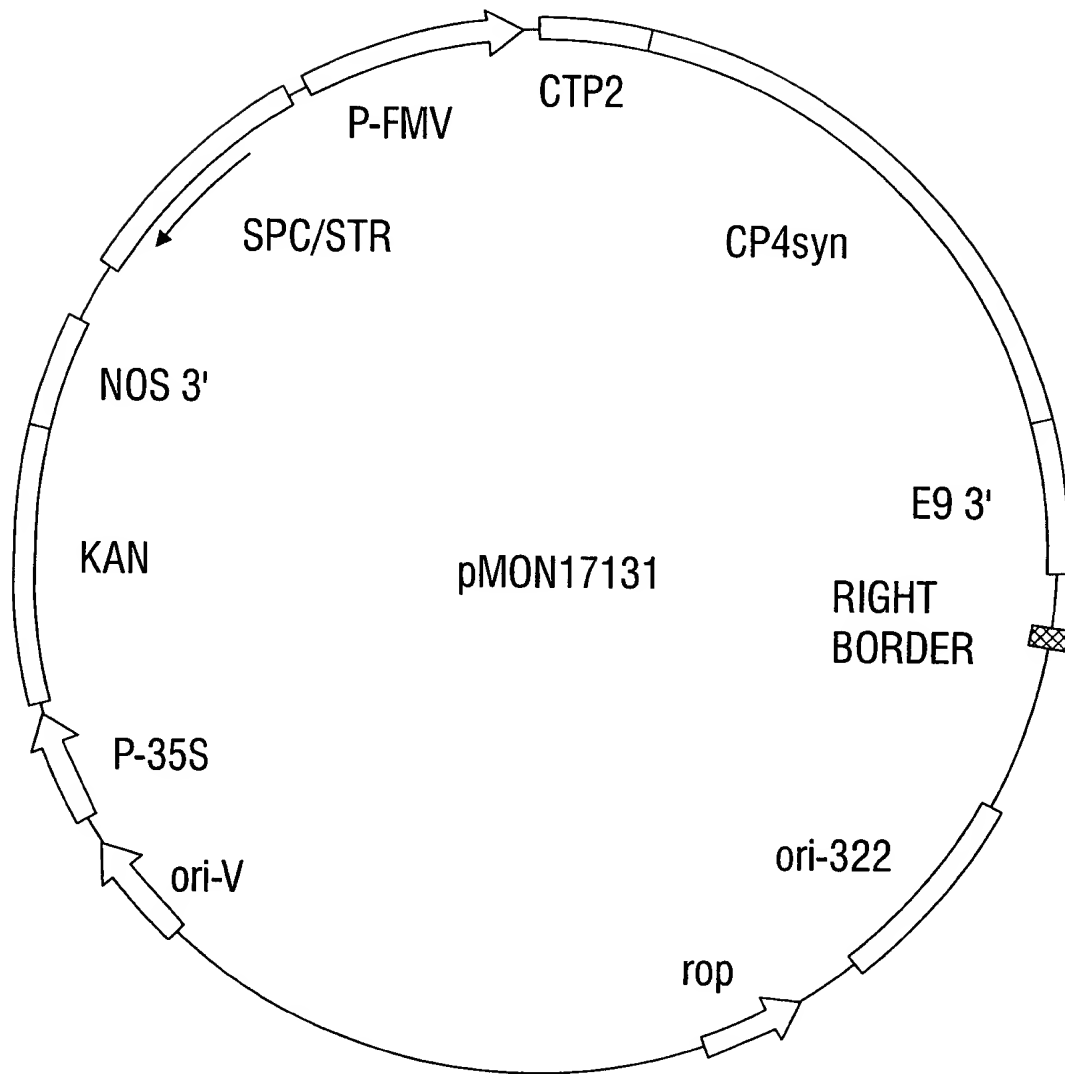


FIG. 14



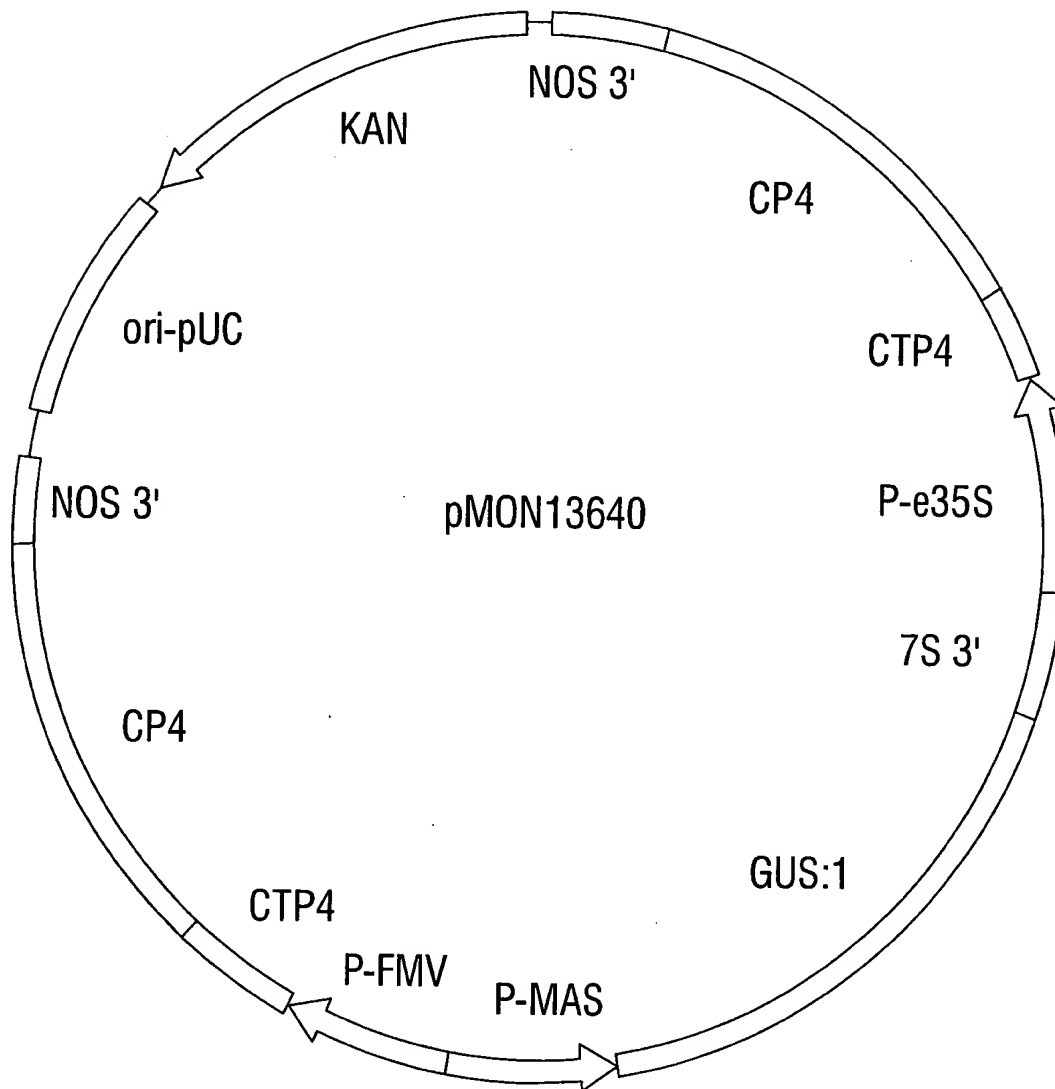


FIG. 15

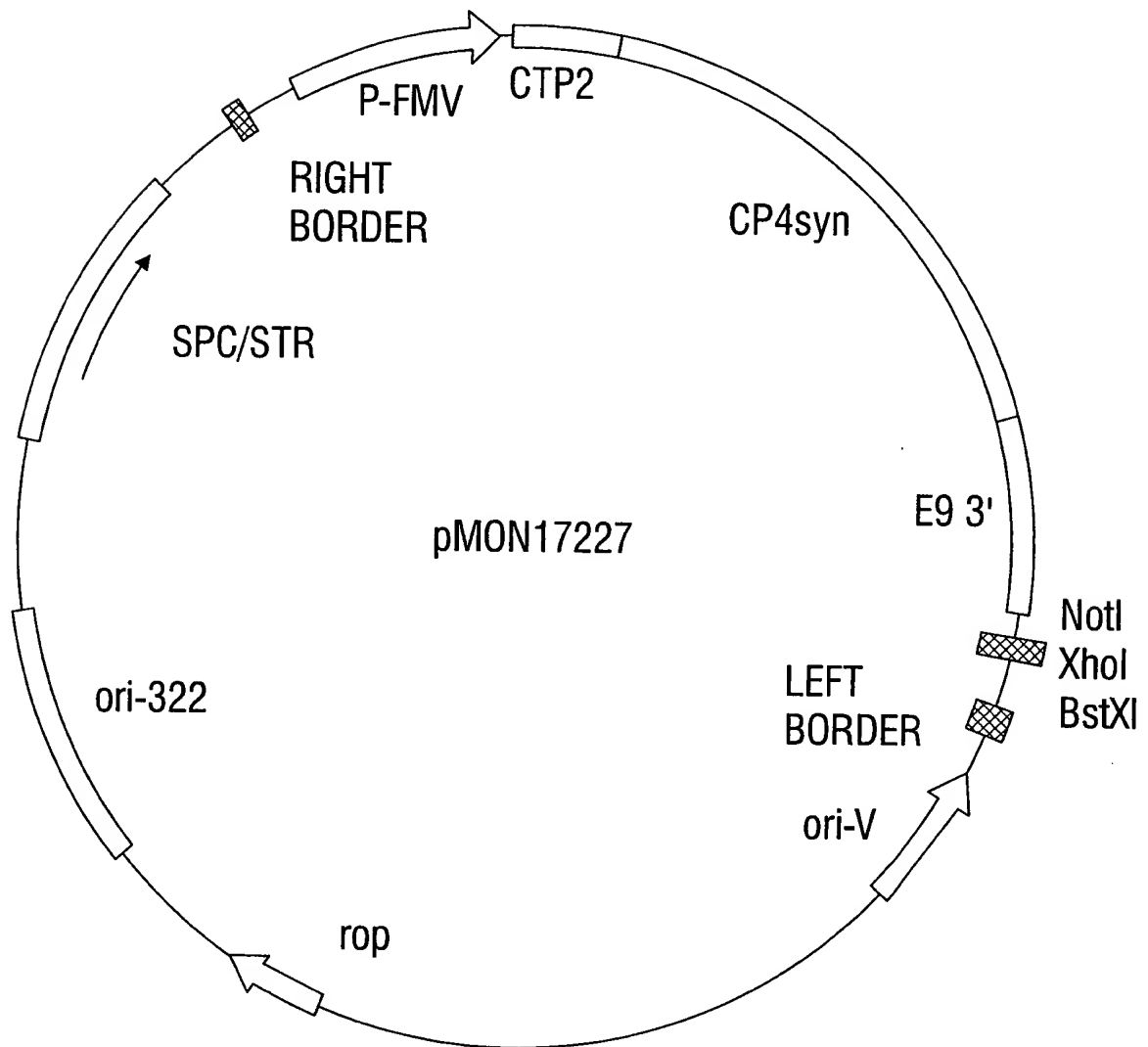


FIG. 16

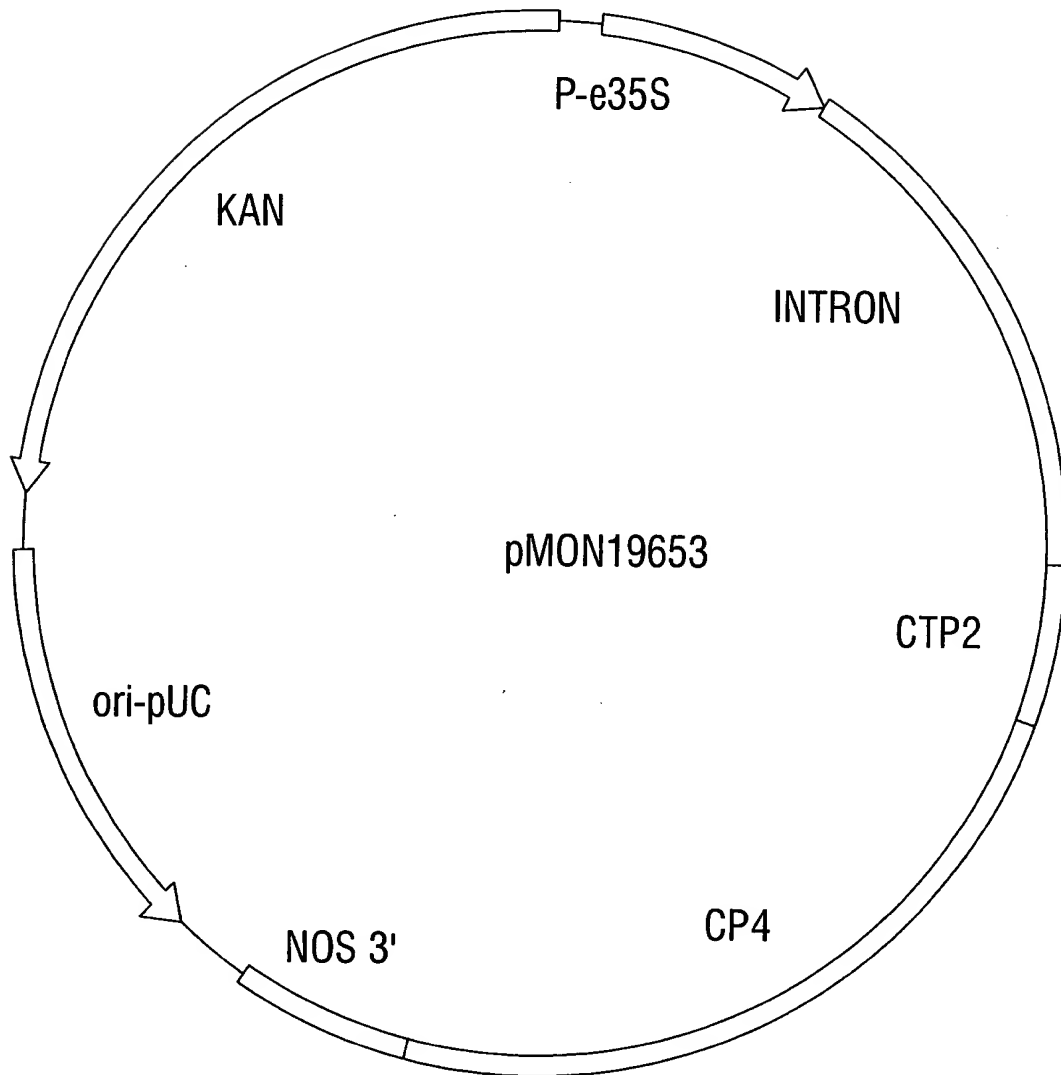


FIG. 17

ATG AAA CGA GAT AAG GTG CAG ACC TTA CAT GGA GAA ATA CAT ATT CCC Met Lys Arg Asp Lys Val Gln Thr Leu His Gly Glu Ile His Ile Pro	1 5 10 15 48
GGT GAT AAA TCC ATT TCT CAC CGC TCT GTT ATG TTT GGC GCG CTA GCG Gly Asp Lys Ser Ile Ser His Arg Ser Val Met Phe Gly Ala Leu Ala	20 25 30 96
GCA GGC ACA ACA GTT AAA AAC TTT CTG CCG GGA GCA GAT TGT CTG Ala Gly Thr Thr Val Val Lys Asn Phe Leu Pro Gly Ala Asp Cys Leu	35 40 144
AGC ACG ATC GAT TGC TTT AGA AAA ATG GGT GTT CAC ATT GAG CAA AGC Ser Thr Ile Asp Cys Phe Arg Arg Lys Met Gly Val His Ile Glu Gln Ser	50 55 60 192
AGC AGC GAT GTC GTG ATT CAC GGA AAA GGA ATC GAT GCC CTG AAA GAG Ser Ser Asp Val Val Ile Ile his Gly Lys Gly Ile Asp Ala Leu Lys Glu	65 70 75 80 240
CCA GAA AGC CTT TTA GAT GTC GGA AAT TCA GGT ACA ACG ATT CGC CTG Pro Glu Ser Ser Leu Leu Asp Val Gly Asn Ser Ser Gly Thr Thr Ile Arg Leu	85 90 95 288
ATG CTC GGA ATA TTG GCG GGC CGT CCT TTT TAC AGC GCG GTA GCC GGA Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly	100 105 110 336

FIG. 18A

GAT GAG AGC ATT GCG AAA CGC CCA ATG AAG CGT GTG ACT GAG CCT TTG	384
Asp Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu	
115 120	
AAA ATG GGG GCT AAA ATC GAC GGC AGA GCC GGC GGA GAG TTT ACA	432
Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Gly Glu Phe Thr	
130 135 140	
CCG CTG TCA GTG AGC GGC GCT TCA TTA AAA GGA ATT GAT TAT GTA TCA	480
Pro Leu Ser Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asp Tyr Val Ser	
145 150 155 160	
CCT GTT GCA AGC GCG CAA ATT AAA TCT GCT GTT TTG CTG GCC GGA TTA	528
Pro Val Ala Ser Ala Ser Gln Ile Lys Ser Ala Val Leu Leu Ala Gly Leu	
165 170 175	
CAG GCT GAG GGC ACA ACT ACT ACA GAG CCC CAT AAA TCT CGG GAC	576
Gln Ala Glu Gly Thr Thr Thr Val Thr Glu Pro His Lys Ser Arg Asp	
180 185 190	
CAC ACT GAG CGG ATG CTT TCT GCT TTT GGC GTT AAG CTT TCT GAA GAT	624
His Thr Glu Arg Met Leu Ser Ala Phe Gly Val Lys Leu Ser Glu Asp	
195 200 205	
CAA ACG AGT GTT TCC ATT GCT GGT GGC CAG AAA CTG ACA GCT GCT GAT	672
Gln Thr Ser Val Ser Ile Ala Gly Gly Gln Lys Leu Thr Ala Ala Asp	
210 215 220	

FIG. 18B

ATT TTT GTT CCT GGA GAC ATT TCT TCA GCC GCG TTT TTC CTT GCT GCT	720
Ile Phe Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Phe Leu Ala Ala	240
225	
GGC GCG ATG GTT CCA AAC AGC AGA ATT GTA TTG AAA AAC GTA GGT TTA	768
Gly Ala Met Val Pro Asn Ser Arg Ile Val Val Leu Lys Asn Val Gly Leu	255
245	
AAT CCG ACT CGG ACA GGT ATT ATT GAT GTC CTT CAA AAC ATG GGG GCA	816
Asn Pro Thr Arg Thr Gly Ile Ile Ile Asp Val Val Leu Gln Asn Met Gly Ala	270
260	
AAA CTT GAA ATC AAA CCA TCT GCT GAT AGC GGT GCA GAG CCT TAT GGA	864
Lys Leu Glu Ile Lys Pro Ser Ala Asp Ser Ser Gly Ala Glu Pro Tyr Gly	285
275	
GAT TTG ATT ATA GAA ACG TCA TCT CTA AAG GCA GTT GAA ATC GGA GGA	912
Asp Leu Ile Ile Glu Thr Ser Ser Leu Lys Ala Val Glu Ile Gly Gly	300
290	
GAT ATC ATT CCG CGT TTA ATT GAT GAG ATC CCT ATC ATC GCG CTT CTT	960
Asp Ile Ile Pro Arg Leu Ile Asp Glu Ile Ile Ile Ala Leu Leu	320
305	
GCG ACT CAG GCG GAA GGA ACC ACC GTT ATT AAG GAC GCG GCA GAG CTA	1008
Ala Thr Gln Ala Glu Gly Thr Thr Val Ile Lys Asp Ala Ala Glu Leu	335
325	
330	

FIG. 18C

AAA GTG AAA GAA ACA AAC CGT ATT GAT ACT GTT GTT TCT GAG CTT CGC	1056
Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Val Ser Glu Leu Arg	
340 345	
AAG CTG GGT GCT GAA ATT GAA CCG ACA GCA GAT GGA ATG AAG GTT TAT	1104
Lys Leu Gly Ala Glu Ile Glu Pro Thr Ala Asp Gly Met Lys Val Tyr	
355 360	
GGC AAA CAA ACG TTG AAA GGC GGC GCT GCA GTG TCC AGC CAC GGA GAT	1152
Gly Lys Gln Thr Thr Leu Lys Gly Gly Ala Ala Val Ser Ser His Gly Asp	
370 375	
CAT CGA ATC GGA ATG ATG CTT GGT ATT GCT TCC TGT ATA ACG GAG GAG	1200
His Arg Ile Gly Met Met Leu Gly Ile Ala Ser Cys Ile Thr Glu Glu	
385 390	
CCG ATT GAA ATC GAG CAC CAC GAT GCC ATT CAC GTT TCT TAT CCA ACC	1248
Pro Ile Glu Ile Glu His Thr Asp Ala Ile His Val Ser Tyr Pro Thr	
405 410	
TTC TTC GAG CAT TTA AAT AAG CTT TCG AAA AAA TCC TGA	1287
Phe Phe Glu His Leu Asn Lys Leu Ser Lys Lys Ser	
420 425	

FIG. 18D

ATG GTA AAT GAA CAA ATC ATT GAT ATT TCA GGT CCG TTA AAG GGC GAA Met Val Asn Glu Gln Ile Ile Asp Ile Ser Gly Pro Leu Lys Gly Glu	1 5 10 15 48
ATA GAA GTG CCG GGC GAT AAG TCA ATG ACA CAC CGT GCA ATC ATG TTG Ile Glu Val Pro Gly Asp Lys Ser Met Thr His Arg Ala Ile Met Leu	20 25 30 96
GCG TCG CTA GCT GAA GGT GTA TCT ACT ATA TAT AAG CCA CTA CTT GGC Ala Ser Leu Ala Glu Gly Val Ser Thr Ile Tyr Lys Pro Leu Leu Gly	35 40 45 144
GAA GAT TGT CGT CGT ACG ATG GAC ATT TTC CGA CAC TTA GGT GTA GAA Glu Asp Cys Arg Arg Thr Met Asp Ile Phe Arg His Leu Gly Val Glu	50 55 60 192
ATC AAA GAA GAT GAT GAA AAA TTA GTT GTG ACT TCC CCA GGA TAT CAA Ile Lys Glu Asp Asp Glu Lys Leu Val Thr Ser Pro Gly Tyr Gln	65 70 75 80 240
GTT AAC ACG CCA CAT CAA GTA TTG TAT ACA GGT AAT TCT GGT ACG ACA Val Asn Thr Pro His Gln Val Thr Tyr Thr Gly Asn Ser Gly Thr Thr	85 90 95 288
ACA CGA TTA TTG GCA GGT TTG TTA AGT GGT TTA GGT AAT GAA AGT GTT Thr Arg Leu Leu Ala Gly Leu Ser Gly Leu Gly Asn Glu Ser Val	100 105 110 336

FIG. 19A



TTG TCT GGC GAT GTT TCA ATT GGT AAA AGG CCA ATG GAT CGT GTC TTG Leu Ser Gly Asp Val Ser Ile Gly Lys Arg Pro Met Asp Arg Val Leu	115 120 125	384
AGA CCA TTG AAA CTT ATG GAT GCG AAT ATT GAA GGT ATT GAA GAT AAT Arg Pro Leu Lys Leu Met Asp Ala Asn Ile Glu Gly Ile Glu Asp Asn	130 135 140	432
TAT ACA CCA TTA ATT ATT AAG CCA TCT GTC ATA AAA GGT ATA AAT TAT Tyr Thr Pro Leu Ile Ile Lys Pro Ser Val Ile Lys Gly Ile Asn Tyr	145 150 155 160	480
CAA ATG GAA GTT GCA AGT GCA CAA GTA AAA AGT GCC ATT TTA TTT GCA Gln Met Glu Val Ala Ser Ala Gln Val Lys Ser Ala Ile Leu Phe Ala	165 170 175	528
AGT TTG TTT TCT AAG GAA CCG ACC ATC ATT AAA GAA TTA GAT GTA AGT Ser Leu Phe Ser Lys Glu Pro Thr Ile Ile Lys Glu Leu Asp Val Ser	180 185	576
CGA AAT CAT ACT GAG ACG ATG TTC AAA CAT TTT AAT ATT CCA ATT GAA Arg Asn His Thr Glu Thr Met Phe Lys His Phe Asn Ile Pro Ile Glu	195 200 205	624
GCA GAA GGG TTA TCA ATT AAT ACA ACC CCT GAA GCA ATT CGA TAC ATT Ala Glu Gly Leu Ser Ile Asn Thr Pro Glu Ala Ile Arg Tyr Ile	210 215 220	672

FIG. 19B

AAA CCT GCA GAT TTT CAT GTT CCT GGC GAT ATT TCA TCT GCA GCG TTC Lys Pro Ala Asp Phe His Val Pro Gly Asp Ile Ser Ser Ala Ala Phe 225 230 235 240	720
TTT ATT GTT GCA GCA CTT ATC ACA CCA GGA AGT GAT GTA ACA ATT CAT Phe Ile Val Ala Ala Leu Ile Thr Pro Gly Ser Asp Val Thr Ile His 245 250 255	768
AAT GTT GGA ATC AAT CAA ACA CGT TCA GGT ATT ATT GAT ATT GTT GAA Asn Val Gly Ile Asn Gln Thr Arg Ser Ser Gly Ile Ile Asp Ile Val Glu 260 265 270	816
AAA ATG GGC GGT AAT ATC CAA CTT TTC AAT CAA ACA ACT GGT GCT GAA Lys Met Gly Gly Asn Ile Gln Leu Phe Asn Thr Thr Gly Ala Glu 275 280 285	864
CCT ACT GCT TCT ATT CGT ATT CAA TAC ACA CCA ATG CTT CAA CCA ATA Pro Thr Ala Ser Ile Arg Ile Gln Tyr Thr Thr Met Leu Gln Pro Ile 290 295 300	912
ACA ATC GAA GGA GAA TTA GTT CCA AAA GCA ATT GAT GAA CTG CCT GTA Thr Ile Glu Gly Glu Leu Val Pro Lys Ala Ile Asp Glu Leu Pro Val 305 310 315 320	960
ATA GCA TTA CTT TGT ACA CAA GCA GTT GGC ACG AGT ACA ATT AAA GAT Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp 325 330 335	1008

FIG. 19C

GCC GAG GAA TTA AAA GTA AAA GAA ACA AAT AGA ATT GAT ACA ACG GCT Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala	1056
GAT ATG TTA AAC TTG TTA GGG TTT GAA TTA CAA CCA ACT AAT GAT GGA Asp Met Leu Asn Leu Leu Leu Phe Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly	1104
TTG ATT ATT CAT CCG TCA GAA TTT AAA ACA AAT GCA ACA GAT ATT TTA Leu Ile Ile His Pro Ser TCA GAA TTT AAA ACA Thr Asn Ala Thr Asp Ile Leu	1152
ACT GAT CAT CGA ATA GGA ATG ATG CTT GCA GTT GCT TGT GTA CTT TCA Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser	1200
AGC GAG CCT GTC AAA ATC AAA CAA TTT GAT GCT GTA AAT GTA TCA TTT Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe	1248
CCA GGA TTT TTA CCA AAA CTA AAG CTT TTA CAA AAT GAG GGA TAA Pro Gly Phe Leu Pro Lys Leu Lys Leu Leu Gln Asn Glu Gly	1293

FIG. 19D

1	PG2982	MSHSASPKPA	TARRSEALTG	50
	LBAA	MSHSASPKPA	TARRSEALTG	
	Agrobacterium CP4	MSHGASSRPA	TARKSSGLSG	
	B. subtilis	.....M	KRDKVQTLHG	
	S. aureus	.....MVNEQ	IIDISGPLKG	
	S. cerevisiae	.....LVYP	FKDIPADQKQ	
	A. nidulans	.....VHP	..GVAHSSNV	
	B. napus	.....K...	VLQPIREISG	
	A. thaliana	.....K...	VLQPIREISG	
	N. tabacum	.....K...	VLQPIKDISG	
	L. esculentum	.....K...	VLXPIKDISG	
	P. hybrida	.....K...	VLQPIKEISG	
	Z. mays	.....AGAEI	VLQPIKEISG	
	S. gallinarum	.....MESL	TLQPIARVDG	
	S. typhimurium	.....MESL	TLQPIARVDG	
	S. typhi	.....MESL	TLQPIARVDG	
	E. coli	.....MESL	TLQPIARVDG	
	K. pneumoniae	.....MESL	TLQPIARVDG	
	Y. enterocolitica	.....MESL	TLHPIALING	
	H. influenzae	.....MEKI	TLAPISAVEG	
	P. multocida	.....MIKDATAI	TLNPISYIEG	
	A. salmonicida	.....NSL	RLEPISRVA	
	B. pertussis	.....MSGLAYL	DLPAARLARG	
	Consensus	.....	.....	

FIG. 20A

51	PG2982	EIRIPGDKSI	SHRSFMFGGL	ASGETRITGL	LEGEDVINTG	RAMQAM.GAK
	LBAA	EIRIPGDKSI	SHRSFMFGGL	ASGETRITGL	LEGEDVINTG	RAMQAM.GAK
	Agrobacterium CP4	TVRIPGDKSI	SHRSFMFGGL	ASGETRITGL	LEGEDVINTG	KAMQAM.GAR
	B. subtilis	EIHIPGDKSI	SHRSVMFGAL	AAGTTTVKNF	LPGADCLSTI	DCFRKM.GVH
	S. aureus	EIEVPGDKSM	THRAIMLASL	AEGVSTIYKP	LLGEDCRRTM	DIFRHL.GVE
	S. cerevisiae	VVIPP <del>GS</del> KSI	SNRALILAAAL	GEGQCKIKNL	LHSDDTKHML	TAVHELKGAT
	A. nidulans	ICAPPGSKSI	SNRALVLAAL	GSGETCRIKNL	LHSDDTTEVML	NALERLGAAT
	B. napus	LIKLP <del>GS</del> KSL	SNRI <del>LL</del> LAAL	SEGTTVVDNL	LNSDDINMYL	DALKKL.GLN
	A. thaliana	LIKLP <del>GS</del> KSL	SNRI <del>LL</del> LAAL	SEGTTVVDNL	LNSDDINMYL	DALKrL.GLN
	N. tabacum	TVKLPGSKSL	SNRI <del>LL</del> LAAL	SKGRTVVDNL	LSSDDIHMYL	GALKTL.GLH
	L. esculentum	TVKLPGSKSL	SNRI <del>LL</del> LAAL	SEGRTVVDNL	LSSDDIHMYL	GALKTL.GLH
	P. hybrida	TVKLPGSKSL	SNRI <del>LL</del> LAAL	SEGTTVVDNL	LSSDDIHMYL	GALKTL.GLH
	Z. mays	TVKLPGSKSL	SNRI <del>LL</del> LAAL	SEGTTVVDNL	LNSDDVHYML	GALRTL.GLS
	S. gallinarum	AINLPGSKSV	SNRALLLAAL	ACGKTVLTNL	LDSDDVHRHML	NALSAL.GIN
	S. typhimurium	AINLPGSKSV	SNRALLLAAL	PCGKTALTNL	LDSDDVHRHML	NALSAL.GIN
	S. typhi	AINLPGSKSV	SNRALLLAAL	ACGKTVLTNL	LDSDDVHRHML	NALSAL.GIN
	E. coli	TINLPGSKTV	SNRALLLAAL	AHGKTVLTNL	LDSDDVHRHML	NALTAL.GVS
	K. pneumoniae	TVNLPGSKSV	SNRALLLAAL	ARGTTVLTNL	LDSDDVHRHML	NALSAL.GVH
	Y. enterocolitica	TVNLPGSKSV	SNRALLLAAL	AEGTTQLNNL	LDSDDIRHML	NALQAL.GVK
	H. influenzae	TINLPGSKSL	SNRALLLAAL	AKGTTKVTLN	LDSDDIRHML	NALKAL.GVR
	P. multocida	EVRLPGSKSL	SNRALLLSAL	AKGKTTLTNL	LDSDDVHRHML	NALKEL.GVT
	A. salmonicida	EVNLPGSKSV	SNRALLLAAL	ARGTTRLTNL	LDSDDIRHML	AALTQL.GVK
	B. pertussis	EVALPGSKSI	SNRVLLAAL	AEGSTEITGL	LDSDDTRVML	AALRQL.GVS
	Consensus	----PG-K--	--R-----L	--G-----L	L---D-----	-----

FIG. 20B

PG2982	IRKEGDVWII	NGVNGCCLLQ	P.....EAA	LDVGNAGTGA	RLTMGLVGTY	150
LBAA	IRKEGDVWII	NGVNGCCLLQ	P.....EAA	LDVGNAGTGA	RLTMGLVGTY	
Agrobacterium CP4	IRKEGDTWII	DGVNGGGLLA	P.....EAP	LDVGNAAATGC	RLTMGLVGTV	
B. subtilis	IEQSSSDVVI	HGKGIDALKE	P.....ESL	LDVGNAGTGA	RLMLGILAGR	
S. aureus	IKEDDEKLW	TSPGYQ.VNT	P.....HQQ	LYTGNAGTGA	RLLAGLLSGL	
S. cerevisiae	ISWEDNGETV	VVEGHGG...	.STLSACADP	LYLGNAGTAS	RFLTSLAALV	
A. nidulans	FSWEEEGEVL	VVNGKGG...	.NLQASSP	LYLGNAGTAS	RFLTSTVATLA	
B. napus	VERDSVNNRA	VVEGCGGIFP	.ASLDSKSDIE	LYLGNAGTAM	RPLTAAVTAA	
A. thaliana	VETDSENNRA	VVEGCGGIFP	.ASIDSKSDIE	LYLGNAGTAM	RPLTAAVTAA	
N. tabacum	VEDDNENQRA	IVEGCGGQFP	.VGKSEEEIQ	LFLGNAGTAM	RPLTAAVTVA	
L. esculentum	VEDDNENQRA	IVEGCGGQFP	.VGKSEEEIQ	LFLGNAGTAM	RPLTAAVTVA	
P. hybrida	VEEDSANQRA	VVEGCGGLFP	.VGKSEEEIQ	LFLGNAGTAM	RPLTAAVTVA	
Z. mays	VEADKAAKRA	VVVGCGGKFP	.VE.DAKEEVQ	LFLGNAGTAM	RPLTAAVTAA	
S. gallinarum	YTLSADRTRC	DITNGGGPLR	AP....GALE	LFLGNAGTAM	RPLAAALCL.	
S. typhimurium	YTLSADRTRC	DITNGGGALR	AP....GALE	LFLGNAGTAM	RPLAAALCL.	
S. typhi	YTLSADRTRC	DITNGGGPLR	AS....GTLE	LFLGNAGTAM	RPLAAALCL.	
E. coli	YTLSADRTRC	EIIGNGGPLH	AE....GALE	LFLGNAGTAM	RPLAAALCL.	
K. pneumoniae	YVLSDDRTRC	EVTGTGGPLQ	AG....SALE	LFLGNAGTAM	RPLAAALCL.	
Y. enterocolitica	YRLSADRTRC	EVDGLGKLV	AE....QPLE	LFLGNAGTAM	RPLAAALCL.	
H. influenzae	YQLSDDKTIC	EIEGLGGAFN	IQ....DNLS	LFLGNAGTAM	RPLTAALCLK	
P. multocida	YQLSEDKSVC	EIEGLGRAFE	WQ....SGLA	LFLGNAGTAM	RPLTAALCLS	
A. salmonicida	YKLSADKTEC	TVHGLGRSFA	VS....APVN	LFLGNAGTAM	RPLCAALCL.	
B. pertussis	VGEVAD..GC	VTIEGVARFP	TE....QAE	LFLGNAGTAF	RPLTAALALM	
Consensus	-----	-----	-----	L--GN--T--	R-----	

FIG. 20C

PG2982	DM.....KT	SFIGDASLSK	RPMGRVLNPL	REMGVQVEAA	DGDRMPLT..	200
LBAA	DM.....KT	SFIGDASLSK	RPMGRVLNPL	REMGVQVEAA	DGDRMPLT..	
Agrobacterium CP4	DF.....DS	TFIGDASLTK	RPMGRVLNPL	REMGVQVKSE	DGDRLPVT..	
B. subtilis	PF.....YS	AVAGDESIK	RPMKRVTEPL	KMGAKIDGR	AGGEFTPL..	
S. aureus	GN.....ES	VLSGDSIGK	RPMDRVLRPL	KLMDANIEG.	IEDNYTPL..	
S. cerevisiae	NST.SSQKYI	VTGNARMQQ	RPIAPLVDSL	RANGTKIEYL	NNEGSLPIKV	
A. nidulans	NS..STVDSS	VLGTGNRMKQ	RPIGDLVDAL	TANVLPNTS	KGRASLPLKI	
B. napus	G....GNASY	VLDGVPRMRE	RPIGDLVVGL	KQLGADVECT	LGTCNCPVVRV	
A. thaliana	G....GNASY	VLDGVPRMRE	RPIGDLVVGL	KQLGADVECT	LGTCNCPVVRV	
N. tabacum	G....GHSRY	VLDGVPRMRE	RPIGDLVDGL	KQLGAEVDCF	LGTCNCPVRI	
L. esculentum	G....GHSRY	VLDGVPRMRE	RPIGDLVDGL	KQLGAEVDCS	LGTCNCPVRI	
P. hybrida	G....GNSRY	VLDGVPRMRE	RPIGDLVDGL	KQLGAEVDCF	LGTCNCPVRI	
Z. mays	G....GNATY	VLDGVPRMRE	RPIGDLVVGL	KQLGADVDCF	LGTCNCPVVRV	
S. gallinarum	....GQNEI	VLTEPRMKE	RPIGHLVDSL	RQGGANIDYL	EQENYPPLRL	
S. typhimurium	....GQNEI	VLTEPRMKE	RPIGHLVDSL	RQGGANIDYL	EQENYPPLRL	
S. typhi	....GQNEI	VLTEPRMKE	RPIGHLVDSL	RQGGANIDYL	EQENYPPLRL	
E. coli	....GSNDI	VLTEPRMKE	RPIGHLVDSL	RLGGAKITYL	EQENYPPLRL	
K. pneumoniae	....GSNDI	VLTEPRMKE	RPIGHLVDSL	RQGGAQIDYL	EQENYPPLRL	
Y. enterocolitica	....GKNDI	VLTEPRMKE	RPIGHLVDSL	RQGGAQIDYL	EQENYPPLRL	
H. influenzae	G.NHEV..EI	ILTGEPRMKE	RPIGHLVDSL	RQAGADIRYL	ENEGYPPLAI	
P. multocida	TPNREGKENI	VLTEPRMKE	RPIGHLVDSL	COAGAEIQYL	EQEGYPPIAI	
A. salmonicida	....GSGEY	MLGGEPRMEE	RPIGHLVDSL	ALKGAHIQYL	KKDGYPPLVW	
B. pertussis	G....GDY	RLSGVPRMHE	RPIGDLVDAL	RQFGAGIEYL	GQAGYPPLRI	
Consensus	-----G-----	-----L	RP-----L	-----	-----	

FIG. 20D

PG2982	201	LIGPK	TANPITYRVP	MASQVKS	LLAGLN	250	TPGVTT
LBAA		LIGPK	TANPITYRVP	MASQVKS	LLAGLN		TPGVTT
Agrobacterium CP4		LRGPK	TPTPITYRVP	MASQVKS	LLAGLN		TPGITT
B. subtilis		SVSGA	SLKGIDYVSP	VASQIKS	LLAGLQ		AEGTTT
S. aureus		IIKPS	VIKGINYQME	VASQVKS	LFASLF		SKEPTI
S. cerevisiae		YTDSVFKG	..GRIELAA	TVSSQVSSI	LMCAPYAE		EPVTLALVG
A. nidulans		AASGGFAG	..GNINLAA	KVSSQVSSL	LMCAPYAK		EPVTLRLVG
B. napus		NANGGLPG	..GKVKLSG	SISSQYLTAL	LMAAP.LA		LGDVEIEII
A. thaliana		NANGGLPG	..GKVKLSG	SISSQYLTAL	LMSAP.LA		LGDVEIEIV
N. tabacum		VSKGGLPG	..GKVKLSG	SISSQYLTAL	LMAAP.LA		LGDVEIEII
L. esculentum		VSKGGLPG	..GKVKLSG	SISSQYLTAL	LMAAP.LA		LGDVEIEII
P. hybrida		VSKGGLPG	..GKVKLSG	SISSQYLTAL	LMAAP.LA		LGDVEIEII
Z. mays		NGIGGLPG	..GKVKLSG	SISSQYLSAL	LMAAP.LP		LGDVEIEII
S. gallinarum		RG..GFIG	..GDIEVDG	SVSSQFLTAL	LMTAP.LA		PKDTIIRVK
S. typhimurium		RG..GFTG	..GDIEVDG	SVSSQFLTAL	LMTAP.LA		PKDTIIRVK
S. typhi		RG..GFIG	..GDIEVDG	SVSSQFLTAL	LMTAP.LA		PEDTIIRVK
E. coli		QG..GFTG	..GNVDVDG	SVSSQFLTAL	LMTAP.LA		PEDTVIRIK
K. pneumoniae		RG..GFTG	..GDVEVDG	SVSSQFLTAL	LMAAP.LA		PQDTVIAIK
Y. enterocolitica		AG..GFRG	..GKLTVDG	SVSSQFLTAL	LMTAP.LA		EQDTEIQIQ
H. influenzae		RNK.GIKG	..GKVKIDG	SISSQFLTAL	LMSAP.LA		ENDTEIEII
P. multocida		RNT.GLKG	..GRIQIDG	SVSSQFLTAL	LMAAP.MA		EADTEIEII
A. salmonicida		DAK.GLWG	..GDVHVDG	SVSSQFLTAF	LMAAPAMA		PVIPRIHIK
B. pertussis		GGGSIRVD	..GPVRVEG	SVSSQFLTAL	LMAAPVLARR		SGQDITIEVV
Consensus		-----	-----	--S-Q----	L-----		-----

FIG. 20E



251	PG2982	TEKMLQGFGA	DLTVETDKGD	VRHIRTGQG	KLVGQ.TIDV	300
	LBAA	TEKMLQGFGA	DLTVETDKDG	VRHIRTGQG	KLVGQ.TIDV	
	Agrobacterium CP4	TEKMLQGFGA	NLTVETDADG	VRTIRLEGRG	KLIGQ.VIDV	
	B. subtilis	TERMLSAFGV	KLSEDQTS..	...VSIAGGQ	KLTA.A.DIFV	
	S. aureus	TETMFKHFN	PIEAEGLS..	..INTTPEAI	RYIKPADFHV	
	S. cerevisiae	GKPISKLYVD	MTIKMMEKFG	IN.VET.STT	EPYTYIIPKG	HYINPSEYVI
	A. nidulans	GKPISQPYID	MTTAMMRSFG	ID..VQKSTT	EEHTYHIPQG	RYVNP AEYVI
	B. napus	DKLISVPYVE	MTLKLMEFVG	VS..AEHSDS	WDRFFVKGGQ	KYKSPGNAYV
	A. thaliana	DKLISVPYVE	MTLKLMEFVG	VS..VEHSDS	WDRFFVKGGQ	KYKSPGNAYV
	N. tabacum	DKLISVPYVE	MTLKLMEFVG	VS..VEHTSS	WDKFLVRGGQ	KYKSPGKAYV
	L. esculentum	DKLISVPYVE	MTLKLMEFVG	VF..VEHSSG	WDRFLVKGGQ	KYKSPGKAFV
	P. hybrida	DKLISVPYVE	MTLKLMEFVG	IS..VEHSSS	WDRFFVVRGGQ	KYKSPGKAFV
	Z. mays	DKLISIPYVE	MTLRLMEFVG	VK..AEHSDS	WDRFYIKGGQ	KYKSPKNAYV
	S. gallinarum	GELVSKPYID	ITLNLTKTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV
	S. typhimurium	GELVSKPYID	ITLNLTKTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV
	S. typhi	GELVSKPYID	ITLNLTKTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV
	E. coli	GDLVSKPYID	ITLNLTKTFG	VE..IEN.QH	YQQFVVKGGQ	SYQSPGTYLV
	K. pneumoniae	GELVSRPYID	ITLHLMKTFG	VE..VEN.QA	YQRFIVRGNG	QYQSPGDYLV
	Y. enterocolitica	GELVSKPYID	ITLHLMKAFG	VD..VVH.EN	YQIFHIKGGQ	TYRSPGIYLV
	H. influenzae	GELVSKPYID	ITLAMMRDFG	VK..VEN.HH	YQKFQVKGNQ	SYISPNKYLV
	P. multocida	GELVSKPYID	ITLKM MQTFG	VE..VEN.QA	YQRFVVKGHQ	QYQSPHRFLV
	A. salmonicida	GELVSKPYID	ITLHIMNSSG	VV..IEH.DN	YKLFYIKGNQ	SIVSPGDFLV
	B. pertussis	GELISKPYIE	ITLNLMARFG	VS..V.RRDG	WRAFTIARDA	VYRGPGRMAI
	Consensus	-----	-----	-----	-----	-----

FIG. 20F

PG2982	PGDPSSTAFP	LVAALLVEGS	DVTIRNVLMN	PTRTGL...	I	LTLQEMGADI	350
LBAA	PGDPSSTAFP	LVAALLVEGS	DVTIRNVLMN	PTRTGL...	I	LTLQEMGADI	
Agrobacterium CP4	PGDPSSTAFP	LVAALLVPGS	DVTILNVLMN	PTRTGL...	I	LTLQEMGADI	
B. subtilis	PGDISSAAFF	LAAGAMVPNS	RIVLKNVGLN	PTRTGI...	I	DVLQNMGAKL	
S. aureus	PGDISSAAFF	IVAALITPGS	DVTIHNVGIN	QIRSGI...	I	DIVEKMGGNI	
S. cerevisiae	ESDASSATYP	LAFAA.MTGT	TVTVPNIGFE	SLOGDARFAR		DVLKPMGCKI	
A. nidulans	ESDASCATYP	LAVAA.VTGT	TCTVPNIGSA	SLOGDARFAV		EVL RPMGCTV	
B. napus	EGDASSASYF	LAGAA.ITGE	TVTVEGCGTT	SLOGDVKFA.		EVLEKMGCKV	
A. thaliana	EGDASSASYF	LAGAA.ITGE	TVTVEGCGTT	SLOGDVKFA.		EVLEKMGCKV	
N. tabacum	EGDASSASYF	LAGAA.VTGG	TVTVEGCGTS	SLOGDVKFA.		EVLEKMGAEV	
L. esculentum	EGDASSASYF	LAGAA.VTGG	TVTVEGCGTS	SLOGDVKFA.		EVLEKMGAEV	
P. hybrida	EGDASSASYF	LAGAA.VTGG	TITVEGCGTN	SLOGDVKFA.		EVLEKMGAEV	
Z. mays	EGDASSASYF	LAGAA.ITGG	TVTVEGCGTT	SLOGDVKFA.		EVLEMMGAKV	
S. gallinarum	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRK	SMQGDIRFA.		DVLEKMGATI	
S. typhimurium	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRK	SMQGDIRFA.		DVLEKMGATI	
S. typhi	EGDASSASYF	LAAGG.IKGG	TVKVTGIGGK	SMQGDIRFA.		DVLHKMGATI	
E. coli	EGDASSASYF	LAAA.IKGG	TVKVTGIGRN	SMQGDIRFA.		DVLEKMGATI	
K. pneumoniae	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRN	SVQGDIRFA.		DVLEKMGATV	
Y. enterocolitica	EGDASSASYF	LAAA.IKGG	TVRVTGIGKQ	SVQGDTKFA.		DVLEKMGAKI	
H. influenzae	EGDASSASYF	LAAGA.IK.G	KVKVTGIGKN	SIQGDRLFA.		DVLEKMGAKI	
P. multocida	EGDASSASYF	LAAA.IK.G	KVKVTGVGKN	SIQGRDLFA.		DVLEKMGAKI	
A. salmonicida	EGDASSASYF	LAAGA.IK.G	KVRVTGIGKH	SI.GDIHFA.		DVLERMGARI	
B. pertussis	EGDASTASYF	LALGA.IGGG	PVRVTGVGED	SIQGDVAFA.		ATLAAMGADV	
Consensus	---D-S---	-----	-----	-----	---	-----MG---	

FIG. 20G

351	PG2982	EVLNARLAGG	EDVADLRVR.	ASKLKGVVVP	PERAPSMIDE	YPVLAIAASF	400
	LBAA	EVLNARLAGG	EDVADLRVR.	ASKLKGVVVP	PERAPSMIDE	YPVLAIAASF	
	Agrobacterium CP4	EVINPRLAGG	EDVADLRVR.	SSTLKGVTVP	EDRAPSMIDE	YPILAVAAAF	
	B. subtilis	EIKPSADSGA	EPYGLIIE.	TSSLKAVEIG	GDIIPRLIDE	IPIIALLATQ	
	S. aureus	QL.FNQTTGA	EPTASIRIQY	TPMLQPITIE	GELVPKAIDE	LPVIALLCCTQ	
	S. cerevisiae	....TQTATS	TTVSGPPV..	...GTLKPLK	HVDMPEMTDA	FLTACVVAAI	
	A. nidulans	....EQTETS	TTVTGSPD..	...GILRATS	KRGYGT.NDR	CVPRCFRTGS	
	B. napus	....SWTENS	VTVTGSPSRDA	FGMRHLRAV.	DVNMNKMPDV	AMTLAVVALF	
	A. thaliana	....SWTENS	VTVTGPPRDA	FGMRHLRAI.	DVNMNKMPDV	AMTLAVVALF	
	N. tabacum	....TWTENS	VTVKGPPRNS	SGMKHLRAV.	DVNMNKMPDV	AMTLAVVALF	
	L. esculentum	....TWTENS	VTVKGPPRNS	SGMKHLRAI.	DVNMNKMPDV	AMTLAVVALF	
	P. hybrida	....TWTENS	VTVKGPPRSS	SGRKHLRAI.	DVNMNKMPDV	AMTLAVVALY	
	Z. mays	....TWTETS	VTVTGPPREP	FGRKHLKAI.	DVNMNKMPDV	AMTLAVVALF	
	S. gallinarum	....TWGDDF	I.....A	CTRGELHAI.	DMDMNHIPDA	AMTIATTALF	
	S. typhimurium	....TWGDDF	I.....A	CTRGELHAI.	DMDMNHIPDA	AMTIATTALF	
	S. typhi	....TWGDDF	I.....A	CTRGELHAI.	DMDMNHIPDA	AMTIATTALF	
	E. coli	....CWGDDY	I.....S	CTRGELNAI.	DMDMNHIPDA	AMTIATAALF	
	K. pneumoniae	....TWGEDY	I.....A	CTRGELNAI.	DMDMNHIPDA	AMTIATAALF	
	Y. enterocolitica	....SWGDDY	I.....E	CSRGELQGI.	DMDMNHIPDA	AMTIATTALF	
	H. influenzae	....TWGEDF	I.....Q	AEHAELNGI.	DMDMNHIPDA	AMTIATTALF	
	P. multocida	....TWGDDF	I.....Q	VEKGNLKGI.	DMDMNHIPDA	AMTIATTALF	
	A. salmonicida	....TWGDDF	I.....E	AEQGPLHGV.	DMDMNHIPDV	GHDHSGQSHC	
	B. pertussis	....RYGPGW	IETRGVRVAE	GGR..LKAF.	DADFNLIPDA	AMTAATLALY	
	Consensus	-----	-----	-----	-----	-----	

FIG. 20H

PG2982	ETVMDGLDEL	RVKESDRLAA	VARGLEANGV	450	DCTEGEMSLT
LBAA	ETVMDGLDEL	RVKESDRLAA	VARGLEANGV		DCTEGEMSLT
Agrobacterium CP4	ATVMNGLEEL	RVKESDRLSA	VANGLKNGV		DCDEGETSLV
B. subtilis	TTVIKDAEEL	KVKETNRIDT	VVSELRLKGA		EIEPTADGMK
S. aureus	TSTIKDAEEL	KVKETNRIDT	TADMLNLLGF		ELQPTNDGLI
S. cerevisiae	TTTIEGIANQ	RVKECNRILA	MATELAKFGV		KTTTEL PDG IQ
A. nidulans	PPVSSGIANQ	RVKECNRIKA	MKDELAKFGV		ICREHDDGLE
B. napus	PTTIRDVASW	RVKETERMIA	ICTELRKLGA		TV. EEGSDYC
A. thaliana	PTTIRDVASW	RVKETERMIA	ICTELRKLGA		TV. EEGSDYC
N. tabacum	PTAIRDVASW	RVKETERMIA	ICTELRKLGA		TV. VEGSDYC
L. esculentum	PTTIRDVASW	RVKETERMIA	ICTELRKLGA		TV. VEGSDYC
P. hybrida	PTAIRDVASW	RVKETERMIA	ICTELRKLGA		TV. EEGPDYC
Z. mays	PTAIRDVASW	RVKETERMVA	IRTELTKLGA		SV. EEGPDYC
S. gallinarum	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA		EV. EEGHDYI
S. typhimurium	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA		EV. EEGHDYI
S. typhi	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA		EV. EEGHDYI
E. coli	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA		EV. EEGHDYI
K. pneumoniae	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA		EV. EEGHDYI
Y. enterocolitica	PTVIRNIYNW	RVKETDRLSA	MATELRKVGA		EV. EEGQDYI
H. influenzae	ETVIRNIYNW	RVKETDRLTA	MATELRKVGA		EV. EEGEDFI
P. multocida	ETVIRNIYNW	RVKETDRLTA	MATELRKVGA		EV. EEGEDFI
A. salmonicida	VPPHSQHLQL	AVRD.DRCTP	CTHGHRAQA		GVSEEGTTFI
B. pertussis	PCRLRNIGSW	RVKETDRIHA	MHTELEKLGA		GV.QSGADWL
Consensus	-----	-V-----R-	-----		-----

FIG. 20I

PG2982	VRGRPDGKGL	G...	GG...	TVATHLDHRI	AMSFLVMGLA	.....	A
LBAA	VRGRPDGKGL	G...	GG...	TVATHLDHRI	AMSFLVMGLA	.....	A
Agrobacterium CP4	VRGRPDGKGL	GNASGA...		AVATHLDHRI	AMSFLVMGLV	.....	S
B. subtilis	VYGKQTLKG.	...	GA...	AVSSHGDHRI	GMMLGIASCI	.....	T
S. aureus	IHPSEFTN.	...	AT....	DI..LTDHRI	GMMLAVACVL	.....	S
S. cerevisiae	VHGLNSIKDL	KVPSDSSGPV		GVCTYDDHRV	AMSFSLLAGM	VNSQNERDEV	
A. nidulans	IDGIDR.SNL	RQPVG.....		GVFCYDDHRV	AFSFSV.L.SL	VTPQ.....	
B. napus	VITP..PAKV	KPA.....		EIDTYDDHRM	AMAFSLAAC.	.....	A
A. thaliana	VITP..PKKV	KTA.....		EIDTYDDHRM	AMAFSLAAC.	.....	A
N. tabacum	IITP..PEKL	NVT.....		EIDTYDDHRM	AMAFSLAAC.	.....	A
L. esculentum	IITP..PEKL	NVT.....		EIDTYDDHRM	AMAFSLAAC.	.....	A
P. hybrida	IITP..PEKL	NVT.....		DIDTYDDHRM	AMAFSLAAC.	.....	A
Z. mays	IITP..PEKL	NVT.....		AIDTYDDHRM	AMAFSLAAC.	.....	A
S. gallinarum	RITP..PAKL	QHA.....		DIGTYNDHRM	AMCFSLVAL.	.....	A
S. typhimurium	RITP..PAKL	QHA.....		DIGTYNDHRM	AMCFSLVAL.	.....	S
S. typhi	RITP..PAKL	QHA.....		DIGTYNDHRM	AMCFSLVAL.	.....	S
E. coli	RITP..PEKL	NFA.....		EIATYNDHRM	AMCFSLVAL.	.....	S
K. pneumoniae	RITP..PLTL	QFA.....		EIGTYNDHRM	AMCFSLVAL.	.....	S
Y. enterocolitica	RVVP..PAQL	IAA.....		EIGTYNDHRM	AMCFSLVAL.	.....	S
H. influenzae	RIQPLALNQF	KHA.....		NIETYNDHRM	AMCFSLIAL.	.....	S
P. multocida	RIQPLNLAQF	QHA.....		ELNI.HDHRM	AMCFALIAL.	.....	S
A. salmonicida	TRDAADPAQA	RRD.....		R..HLQRSRI	AMCFSLVAL.	.....	S
B. pertussis	EVAPPEPGGW	RDA.....		HIGTWDDHRM	AMCFLLAAF.	.....	S
Consensus	-----	-----	-----	-----R-	-----	-----	-----

FIG. 20J

501	PG2982	EKPVTVDDSN	MIATSFPEFM	DMMPGLGAKI	ELSIL	538
	LBAA	EKPVTVDDSN	MIATSFPEFM	DMMPGLGAKI	ELSIL	
	Agrobacterium CP4	ENPVTVDDAT	MIATSFPEFM	DLMAGLGAKI	ELSDTKAA	
	B. subtilis	EEPIEIEHTD	AIHVSYPYTF	EHLNKLKSKS		
	S. aureus	SEPVKIKQFD	AVNVSPGFL	PKLKLQNEG		
	S. cerevisiae	ANPVRILERH	CTGKTWPGWW	DVLH		
	A. nidulans	..PTLILEKE	CVGKTWPGWW	DTLRQLFKV		
	B. napus	DVPVTIKDPG	CTRKTFPDYF	QVLESITKH		
	A. thaliana	DVPITINDSG	CTRKTFPDYF	QVLERITKH		
	N. tabacum	DVPVTIKDPG	CTRKTFPNYF	DVLQQYSKH		
	L. esculentum	DVPVTIKNPG	CTRKTFPDYF	EVLQKYSKH		
	P. hybrida	DVPVTINDPG	CTRKTFPNYF	DVLQQYSKH		
	Z. mays	EVPVTIRDPG	CTRKTFPDYF	DVLSTFVKV		
	S. gallinarum	DTPVTIILDPK	CTAKTFPDYF	EQLARMSTPA		
	S. typhimurium	DTPVTIILDPK	CTAKTFPDYF	EQLARMSTPA		
	S. typhi	DTPVTIILDPK	CTAKTFPDYF	EQLARMSTPA		
	E. coli	DTPVTIILDPK	CTAKTFPDYF	EQLARISQAA		
	K. pneumoniae	DTPVTIILDPK	CTAKTFPDYF	GQLARISTLA		
	Y. enterocolitica	DTPVTIILDPK	CTAKTFPDYF	EQLARLSQIA		
	H. influenzae	NTPVTIILDPK	CTAKTFPTFF	NEFE...KI	CLKN	
	P. multocida	KTSVTIILDPK	CTAKTFPTFL	ILFTLNTREV	AYR	
	A. salmonicida	DIAVTINDPG	CTSKTFPDYF	DKLASVSQAV		
	B. pertussis	PAAVRILDPG	CVSKTFPDYF	DVYAGLLAAR	D	
	Consensus	-----	-----P	-----	-----	

FIG. 20K

FIG. 21A

TTT CGG GCC ATG GGA GCA GAA ATC AGC GAA CTA AAT TCA GAA AAA ATC	532
Phe Arg Ala Met Gly Ala Glu Ile Ser Glu Leu Asn Ser Glu Lys Ile	75 80 85
ATC GTT CAG GGT CGG GGT CTG GGA CAG TTG CAG GAA CCC AGT ACC GTT	580
Ile Val Gln Gly Arg Gly Leu Gly Gln Leu Glu Pro Ser Thr Val	90 95 100
TTG GAT GCG GGG AAC TCT GGC ACC ACC ATG CGC TTA ATG TTG GGC TTG	628
Leu Asp Ala Gly Asn Ser Gly Thr Thr Met Arg Leu Met Leu Gly Leu	105 110 115
CTA GCC GGG CAA AAA GAT TGT TTA TTC ACC GTC ACC GGC GAT GAT TCC	676
Leu Ala Gly Gln Lys Asp Cys Leu Phe Thr Val Thr Gly Asp Ser	120 125 130
CTC CGT CAC CGC CCC ATG TCC CGG GTA ATT CAA CCC TTG CAA CAA ATG	724
Leu Arg His Arg Pro Met Ser Arg Val Ile Gln Pro Leu Gln Gln Met	135 140 145 150
GGG GCA AAA ATT TGG GCC GCG AGT AAC GGC AAG TTT GCG CCG CTG GCA	772
Gly Ala Lys Ile Trp Ala Arg Ser Asn Gly Lys Phe Ala Pro Leu Ala	155 160 165
GTC CAG GGT AGC CAA TTA AAA CCG ATC CAT TAC CAT TCC CCC ATT GCT	820
Val Gln Gly Ser Gln Leu Lys Pro Ile His Tyr His Ser Pro Ile Ala	170 175 180

FIG. 21B



TCA GCC CAG GTA AAG TCC TGC CTG TTG CTA GCG GGG TTA ACC ACC GAG	868
Ser Ala Gln Val Lys Ser Cys Leu Leu Ala Gly Leu Thr Thr Glu	
	185
	190
	195
GGG GAC ACC ACG GTT ACA GAA CCA GCT CTA TCC CGG GAT CAT AGC GAA	916
Gly Asp Thr Thr Val Thr Glu Pro Ala Leu Ser Arg Asp His Ser Glu	
	200
	205
	210
CGC ATG TTG CAG GCC TTT GGA GCC AAA TTA ACC ATT GAT CCA GTA ACC	964
Arg Met Leu Gln Ala Phe Thr Gln Ala Lys Leu Thr Ile Asp Pro Val Thr	
	215
	220
	225
CAT AGC GTC ACT GTC CAT GGC CCG GCC CAT TTA ACG GGG CAA CGG GTG	1012
His Ser Val Thr Val His His Ala Pro Ala His Leu Thr Gly Gln Arg Val	
	235
	240
	245
GTG GTG CCA GGG GAC ATC AGC TCG GCG GCC TTT TGG TTA GTG GCG GCA	1060
Val Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Trp Leu Val Ala Ala	
	250
	255
	260
TCC ATT TTG CCT GGA TCA GAA TTG TTG GTG GAA AAT GTA GGC ATT AAC	1108
Ser Ile Leu Pro Gly Ser Glu Leu Leu Val Val Asn Val Gly Ile Asn	
	265
	270
	275
CCC ACC AGG ACA GGG GTG TTG GAA GTG TTG GCC CAG ATG GGG GCG GAC	1156
Pro Thr Arg Thr Gly Val Leu Glu Val Leu Ala Gln Met Gly Ala Asp	
	280
	285
	290

FIG. 21C

ATT ACC CCG GAG AAT GAA CGA TTG GTA ACG GGG GAA CCG GTA GCA GAT Ile Thr Pro Glu Asn 300 295	1204
CTG CGG GTT AGG GCA AGC CAT CTC CAG GGT TGC ACC TTC GGC GGC GAA Leu Arg Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly Gly Glu 315 320 325	1252
ATT ATT CCC CGA CTG ATT GAT GAA ATT CCC ATT TTG GCA GTG GCG GCG Ile Ile Pro Arg Arg Leu Ile Asp Glu Ile Pro Ile Leu Ala Val Ala Ala 330 335 340	1300
GCC TTT GCA GAG GGC ACT ACC CGC ATT GAA GAT GCC GCA GAA CTG AGG Ala Phe Ala Glu Glu Thr Thr Arg Ile Glu Asp Ala Ala Glu Leu Arg 345 350 355	1348
GTT AAA GAA AGC GAT CGC CTG GCG GCC ATT GCT TCG GAG TTG GGC AAA Val Lys Glu Ser Asp Arg Leu Ala Ala Ile Ala Ser Glu Leu Gly Lys 360 365 370	1396
ATG GGG GCC AAA GTC ACC GAA TTT GAT GAT GGC CTG GAA ATT CAA GGG Met Gly Ala Lys Val Thr Glu Phe Asp Asp Gly Leu Glu Ile Gln Gly 375 380 385 390	1444
GGA AGC CCG TTA CAA GGG GCC GAG GTG GAT AGC TTG ACG GAT CAT CGC Gly Ser Pro Leu Gln Gly Ala Glu Val Asp Ser Leu Thr Asp His Arg 395 400 405	1492

FIG. 21D

ATT GCC ATG GCG TTG GCG ATC GCC GCT TTA GGT AGT GGG GGG CAA ACA Ile Ala Met Ala Leu Ala Ile Ala Ala 415 410	1540
ATT ATT AAC CGG GCG GAA GCG GCC GCC ATT TCC TAT CCA GAA TTT TTT Ile Ile Asn Arg Ala Glu Ala Ala Ala Ile Ser Tyr Pro Glu Phe Phe 425 430 435	1588
GGC ACG CTA GGG CAA GTT GCC CAA GGA TAAAGTTAGA AAAACTCCTG Gly Thr Leu Gly Gln Val Ala Gln Gly 440 445	1635
GGCGGTTTGT AAATGTTTTTA CCAAGGTAGT TTGGGGTAAAGGCCCCAGCA AGTGTGCCA	1695
GGGTAATTTA TCCGCAATTG ACCAATCGGC ATGGACCGTA TCGTTCAAAC TGGGTAATTC	1755
TCCCTTTAAT TCCTTAAAG CTCGCTTAA ACTGCCCAAC GTATCTCCGT AATGGCGAGT	1815
GAGTAGAAGT AATGGGGCCA AACGGCGATC GCCACGGGAA ATTAAGCCT GCATCACTGA	1875
CCACTTATAA CTTTCGGGA	1894

FIG. 21E

TTTAAAAACA	ATGAGTTAA	AAATTATTT	TCTGGCACAC	GCGCTTTTT	TGCATTTTT	60
CTCCCATTTT	TCCGGCACAA	TAAGTTGGT	TTTATAAAG	GAAATG	ATG ATG ACG	115
				Met Met Thr		
AAT ATA TGG CAC ACC GCG CCC GTC TCT GCG CTT TCC GGC GAA ATA ACG						163
Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly Glu Ile Thr						
ATA TGC GGC GAT AAA TCA ATG TCG CAT CGC GCC TTA TTA TTA GCA GCG						211
Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu Ala Ala						
TTA GCA GAA GGA CAA ACG GAA ATC CGC GGC TTT TTA GCG TGC GCG GAT						259
Leu Ala Glu Gly Gln Thr Thr Glu Ile Arg Gly Phe Leu Ala Cys Ala Asp						
TGT TTG GCG ACG CGG CAA GCA TTG CGC GCA TTA GGC GTT GAT ATT CAA						307
Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val Asp Ile Gln						
AGA GAA AAA GAA ATA GTG ACG ATT CGC GGT GTG GGA TTT CTG GGT TTG						355
Arg Glu Lys Ile Ile Val Thr Ile Arg Gly Val Gly Phe Leu Gly Leu						

FIG. 22A

CAG CCG CCG AAA GCA CCG TTA AAT ATG CAA AAC AGT GGC ACT AGC ATG Gln Pro Pro Lys Ala Pro Ile Leu Asn Met Gln Asn Ser Gly Thr Ser Met 85 90 95	403
CGT TTA TTG GCA GGA ATT TTG GCA GCG CAG CGC TTT GAG AGC GTG TTA Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu Ser Val Leu 100 105 110	451
TGC GGC GAT GAA TCA TTA GAA AAA CGT CCG ATG CAG CGC ATT ATT ACG Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg Ile Ile Thr 120 125	499
CCG CTT GTG CAA ATG GGG GCA AAA ATT GTC AGT CAC AGC AAT TTT ACG Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser Asn Phe Thr 135 140 145	547
GCG CCG TTA CAT ATT TCA GGA CCG CCG CTG ACC GGC ATT GAT TAC GCG Ala Pro Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile Asp Tyr Ala 150 155 160	595
TTA CCG CTT CCC AGC GCG CAA TTA AAA AGT TGC CTT ATT TTG GCA GGA Leu Pro Leu Pro Ser Ala Gln Leu Lys Ser Cys Leu Ile Leu Ala Gly 165 170 175	643
TTA TTG GCT GAC GGT ACC ACG CGG CTG CAT ACT TGC GGC ATC AGT CGC Leu Leu Ala Asp Gly Thr Thr Arg Leu His Thr Cys Gly Ile Ser Arg 180 185 190 195	691

FIG. 22B

GAC CAC ACG GAA CGC ATG TTG CCG CTT TTT GGT GGC GCA CTT GAG ATC	739
Asp His Thr Glu Arg Met Leu Pro Leu Phe Gly Gly Ala Leu Glu Ile	210
AAG AAA GAG CAA ATA ATC GTC ACC GGT GGA CAA AAA TTG CAC GGT TGC	787
Lys Lys Glu Gln Ile Ile Val Thr Gly Gln Lys Leu His Gly Cys	225
GTG CTT GAT ATT GTC GGC GAT TTG TCG GCG GCG GCG TTT TTT ATG GTT	835
Val Leu Asp Ile Val Gly Asp Leu Ser Ala Ala Ala Phe Phe Met Val	240
GCG GCT TTG ATT GCG CCG CGC GCG GAA GTC GTT ATT CGT AAT GTC GGC	883
Ala Ala Leu Ile Ala Pro Arg Ala Glu Val Ile Arg Asn Val Gly	255
ATT AAT CCG ACG CCG GCG GCA ATC ATT ACT TTG CAA AAA ATG GGC	931
Ile Asn Pro Thr Arg Ala Ile Ile Thr Leu Leu Gln Lys Met Gly	275
GGA CGG ATT GAA TTG CAT CAT CAG CGC TTT TGG GGC GCC GAA CCG GTG	979
Gly Arg Ile Glu Leu His His Gln Arg Phe Trp Gly Ala Glu Pro Val	280 285 290
GCA GAT ATT GTT GTT TAT CAT TCA AAA TTG CGC GGC ATT ACG GTG GCG	1027
Ala Asp Ile Val Val Tyr His Ser Lys Leu Arg Gly Ile Thr Val Ala	295 300 305

FIG. 22C

CCG GAA TGG ATT GCC AAC GCG ATT GAT GAA TTG CCG ATT TTT TTT ATT	1075
Pro Glu Trp Ile Ala Asn Ala Ile Asp Glu Leu Pro Ile Phe Phe Ile	
310 315 320	
GCG GCA GCT TGC GCG GAA GGG ACG ACT TTT GTG GGC AAT TTG TCA GAA	1123
Ala Ala Cys Ala Glu Gly Thr Thr Phe Val Gly Asn Leu Ser Glu	
325 330 335	
TTG CGT GTG AAA GAA TCG GAT CGT TTA GCG GCG ATG GCG CAA AAT TTA	1171
Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Met Ala Gln Asn Leu	
340 345 350 355	
CAA ACT TTG GCG GTG GCG TGC GAC GTT GGC GCC GAT TTT ATT CAT ATA	1219
Gln Thr Leu Gly Val Ala Cys Asp Val Gly Ala Ala Asp Phe Ile His Ile	
360 365 370	
TAT GGA AGA AGC GAT CCG CAA TTT TTA CCG GCG CGG GTG AAC AGT TTT	1267
Tyr Gly Arg Ser Asp Arg Gln Phe Leu Pro Ala Arg Val Asn Ser Phe	
375 380 385	
GGC GAT CAT CCG ATT GCG ATG AGT TTG GCG GTG GCA GGT GTG CGC GCG	1315
Gly Asp His Arg Ile Ala Met Ser Leu Ala Val Ala Gly Val Arg Ala	
390 395 400 405	
GCA GGT GAA TTA TTG ATT GAT GAC GCG GTG GCG GCG GGT TCT ATG	1363
Ala Gly Glu Leu Ile Asp Gly Ala Val Ala Ala Val Ser Met	
405 410 415	

FIG. 22D

CCG CAA TTT CGC GAT TTT GCC GCC GCA ATT GGT ATG AAT GTA GGA GAA	1411
Pro Gln Phe Arg Asp Phe Ala Ala Ile Gly Met Asn Val Gly Glu	420 425 430 435
AAA GAT GCG AAA AAT TGT CAC GAT TGATGGTCCT AGCGGTGTTG GAAAAGGCAC	1465
Lys Asp Ala Lys Asn Cys His Asp	440
GGTGGCGCAA GCTT	1479

FIG. 22E



FIG. 23A

1	PG2982	MS	HSASPKPATA	RRSEALTGEI	RIPGDKSISH	40
	LBAA	MS	HSASPKPATA	RRSEALTGEI	RIPGDKSISH	
	Agrobacterium CP4	MS	HGASSRPATA	RKSSGLSGTV	RIPGDKSISH	
	Synechocystis sp. PCC6803	MALLSLNNHQ	SHQRLTVNPP	AQGVALTGRL	RVPGDKSISH	
	B. subtilis		.....MKR	DKVQTLHGEI	HIPGDKSISH	
	D. nodosus		.....MMTNIWHT	APVSALSGEI	TICGDKSMTH	
	S. aureus		.....MVNEQII	DISGPLKGEI	EVPGDKSMTH	
	Consensus		-----	-----L-G--	-I-GDKS--H	
41	PG2982	RSFMFGGLAS	GETRITGLLE	GEDVINTGRA	MQAMGAKI.R	80
	LBAA	RSFMFGGLAS	GETRITGLLE	GEDVINTGRA	MQAMGAKI.R	
	Agrobacterium CP4	RSFMFGGLAS	GETRITGLLE	GEDVINTGKA	MQAMGARI.R	
	Synechocystis sp. PCC6803	RALMLGAIAT	GETIIEGLLL	GEDPRSTAHC	FRAMGAEISE	
	B. subtilis	RSVMFGALAA	GTTTVKNFLP	GADCLSTIDC	FRKMGVHI.E	
	D. nodosus	RALLLAALAE	GQTEIRGFLA	CADCLATRQA	LRLGVDI.Q	
	S. aureus	RAIMLASLAE	GVSTIYKPLL	GEDCRRTMDI	FRHLGVEI.K	
	Consensus	R--MF---A-	G---I---L-	--D---T---	---MG---I--	
81	PG2982	KEGDVWIING	VNGGCLLQPE	AALDFGNAGT	GARLTMGLVG	120
	LBAA	KEGDVWIING	VNGGCLLQPE	AALDFGNAGT	GARLTMGLVG	
	Agrobacterium CP4	KEGDTWIIDG	VNGGGLLAPE	APLDFGNAAT	GCRLTMGLVG	
	Synechocystis sp. PCC6803	LNSEKIIVQG	RGLGQLQEPS	TVLDAGNSGT	TMRLMLGLLA	
	B. subtilis	QSSSDVVIHG	KGIDALKEPE	SLLDVGNST	TIRMLGILA	
	D. nodosus	REKEIVTIRG	VGFLGLOPPK	APLNMQNSGT	SMRLLAGILA	
	S. aureus	EDDEKLVVTS	PGYQ.VNTPH	QVLYTGNST	TTRLLAGLLS	
	Consensus	-----I--	-G-----P-	--L---N--T	--RL--G---	

FIG. 23B

PG2982	121	TY.DMKTSFI	GDASLSKRPM	GRVLNPLRM	GVQVEAADGD	160
LBAA		TY.DMKTSFI	GDASLSKRPM	GRVLNPLRM	GVQVEAADGD	
Agrobacterium CP4		VY.DFDSTFI	GDASLTKRPM	GRVLNPLRM	GVQVKSEDDG	
Synechocystis sp. PCC6803		GQKDCCLFTVT	GDDSLRHRPM	SRVIQPLQQM	GAKIWARNSNG	
B. subtilis		G.RPFYSAVA	GDESIKRPM	KRVTEPLKKM	GAKIDGRAGG	
D. nodosus		AQR.FESVLC	GDESLEKRPM	QRIITPLVQM	GAKIVSHSNF	
S. aureus		GLGN.ESVLS	GDVSIGKRPM	DRVLRPLKLM	DANIEGIEDN	
Consensus		-----	GD-S---RPM	-RV--PL--M	---I-----	

PG2982	161	RMPLTLIGPK	TANPITYRVP	MASQVKSASV	LLAGLNTPGV	200
LBAA		RMPLTLIGPK	TANPITYRVP	MASQVKSASV	LLAGLNTPGV	
Agrobacterium CP4		RLPVTLRGPK	TPTPITYRVP	MASQVKSASV	LLAGLNTPGI	
Synechocystis sp. PCC6803		KFAPLAVQGS	QLKPIHYHSP	IASAQVKSCL	LLAGLTTEGD	
B. subtilis		EFTPLSVSGA	SLKGIDYVSP	VASAQIKSAV	LLAGLQAEGT	
D. nodosus		T.APLHISGR	PLTGIDYALP	LPSAQLKSCL	ILAGLLADGT	
S. aureus		.YTPLIIKPS	VIKGINYQME	VASAQVKSAT	LFASLFSKEP	
Consensus		-----	----I-Y----	--SAQ-KS--	-LA-L-----	

PG2982	201	TTVIEPVMTR	DHTEKMLQGF	.....	GADLT	VETDKDGVRRH	240
LBAA		TTVIEPVMTR	DHTEKMLQGF	.....	GADLT	VETDKDGVRRH	
Agrobacterium CP4		TTVIEPIMTR	DHTEKMLQGF	.....	GANLT	VETDADGVRT	
Synechocystis sp. PCC6803		TTVTEPALSR	DHSERMLQAF	.....	GAKLT	IDPVTHSV..	
B. subtilis		TTVTEPHKSR	DHTERMLSAF	.....	GVKLS	EDQT..SV..	
D. nodosus		TRLHTCGISR	DHTERMLPLF	.....	GGALE	IKK..EQI..	
S. aureus		TIIEKELDVSR	NHTETMFKHF	.....	NIPIEAEGLS	INTTPEAIRY	
Consensus		T-----R	-H-E-ML--F	-----L-	-----V--		

FIG. 23C

241  
IRITGQGKLV GQTIDVPGDP 280  
IRITGQGKLV GQTIDVPGDP LLVEGSDVTI  
IRLEGRGKLT GQVIDVPGDP SSTAFLPLVAA LLVEGSDVTI  
.TVHGPAHLT GQRVVVPGDI SSTAFLPLVAA LLVPGSDVTI  
.SIAGGQKLT AADIFVPGDI SSAAFwLVAA SILPGSELLV  
.IVTGGQKLH GCVLDIVGDL SSAAFFLAAG AMVPNSRIVL  
IKPAD.....FHVPGDI SAAFFFMVAA LIAPRAEVVI  
-----S--AF---A- LITPGSDVTI  
-----V-GD- ----

PG2982  
LBAA  
Agrobacterium CP4  
Synechocystis sp. PCC6803  
B. subtilis  
D. nodosus  
S. aureus  
Consensus

281  
RNVLMNPTRT GLILTLQEMG 320  
RNVLMNPTRT GLILTLQEMG AGGEDVADLR  
LNVLMNPTRT GLILTLQEMG ADIEVLNARL AGGEDVADLR  
ENVGINPTRT GVLEVLQMG ADIEVINPRL AGGEDVADLR  
KNVGLNPTRT GIIDVLQNMG ADITPENERL VTGEPVADLR  
RNVGINPTRA AIITLLQKMG AKLEIKPSAD SGAEPYGDLI  
HNVGINQTRS GIIDIVEKMG GRIELHHQRF WGAEPVADIV  
-NV--N-IR- GNIQLFNQT. TGAEPTASIR  
-----MG -----E-----

PG2982  
LBAA  
Agrobacterium CP4  
Synechocystis sp. PCC6803  
B. subtilis  
D. nodosus  
S. aureus  
Consensus

321  
VR.ASKLKGV VPPERAPSM 360  
VR.ASKLKGV VPPERAPSM IDEYPLVLAIA ASFAEGETVM  
VR.SSTLKGV TVPEDRAPSM IDEYPLVLAIA ASFAEGETVM  
VR.ASHLQGC TFGGEIIPRL IDEYPIILAVA AFAEAGATVM  
IE.TSSLKAV EIGGDIIPRL IDEIPIILAVA AFAEAGTTTRI  
VY.HSKLRGI TVAPEWIANA IDEIPIALL ATQAEGTTVI  
IQYTPMLQPI TIEGELVPKA IDELPIFFIA AACAEGTTFV  
V-----L--- ----E----- IDELPVIAL CTQAVGTSTI  
-----A-G----

PG2982  
LBAA  
Agrobacterium CP4  
Synechocystis sp. PCC6803  
B. subtilis  
D. nodosus  
S. aureus  
Consensus

FIG. 23D

PG2982	361	DGLDELRVKE	SDRLAAVARG	LEANGVDCTE	GEMSLTVRGR	400
LBAA		DGLDELRVKE	SDRLAAVARG	LEANGVDCTE	GEMSLTVRGR	
Agrobacterium CP4		NGLEELRVKE	SDRLSAVANG	LKLNQVDCDE	GETSLVVRGR	
Synechocystis sp. PCC6803		EDAAELRVKE	SDRLAAIASE	LKMGAKVTE	FDDGLEIQGG	
B. subtilis		KDAAELRVKE	TNRIDTVSE	LRKLGAEIEP	TADGMKVYVK	
D. nodosus		GNLSELRVKE	SDRLAAMAQN	LQTLGVACDV	GADFIHIYGR	
S. aureus		KDAEELRVKE	TNRIDTTADM	LNLGFELOP	TNDGLIIHPS	
Consensus		---EL-VKE	--R-----	L---G----	-----V----	

PG2982	401	PDGKGLG...	GGTVATHLDH	RIAMSFLVMG	LAAEKPVTVD	440
LBAA		PDGKGLG...	GGTVATHLDH	RIAMSFLVMG	LAAEKPVTVD	
Agrobacterium CP4		PDGKGLGNAS	GAAVATHLDH	RIAMSFLVMG	LVSENPVTVD	
Synechocystis sp. PCC6803		SPLQ.....	GAEVDSLTDH	RIAMALIAAA	LGSGGQTIIN	
B. subtilis		QTLK.G....	GAAVSSHGDH	RIGMMLGAS	CITEEPIEIE	
D. nodosus		SDRQFL....	PARVNSFGDH	RIAMSLAVAG	VRAAGELLID	
S. aureus		E.....FK	TNATDILTTH	RIGMMLAVAC	VLSSEPVKIK	
Consensus		-----	-----DH	RI-M-L-V--	-----I--	

PG2982	441	DSNMIATSFP	EFMDMMPGLG	AKIELSIL..	...	437
LBAA		DSNMIATSFP	EFMDMMPGLG	AKIELSIL..	...	
Agrobacterium CP4		DATMIATSFP	EFMDLMAGLG	AKIELSDTKA	A..	
Synechocystis sp. PCC6803		RAEAAAISYP	EFFGTLGQVA	QG*	...	
B. subtilis		HTDAIHVSYP	TFFEHLNKL	KKS	.....	
D. nodosus		DGAVAASVMP	QFRDFAAAIG	MNVGEKDAKN	CHD	
S. aureus		QFDVAVNSFP	GFLPKLKLQ	NEG	.....	
Consensus		-----S-P	-F-----	-----	----	

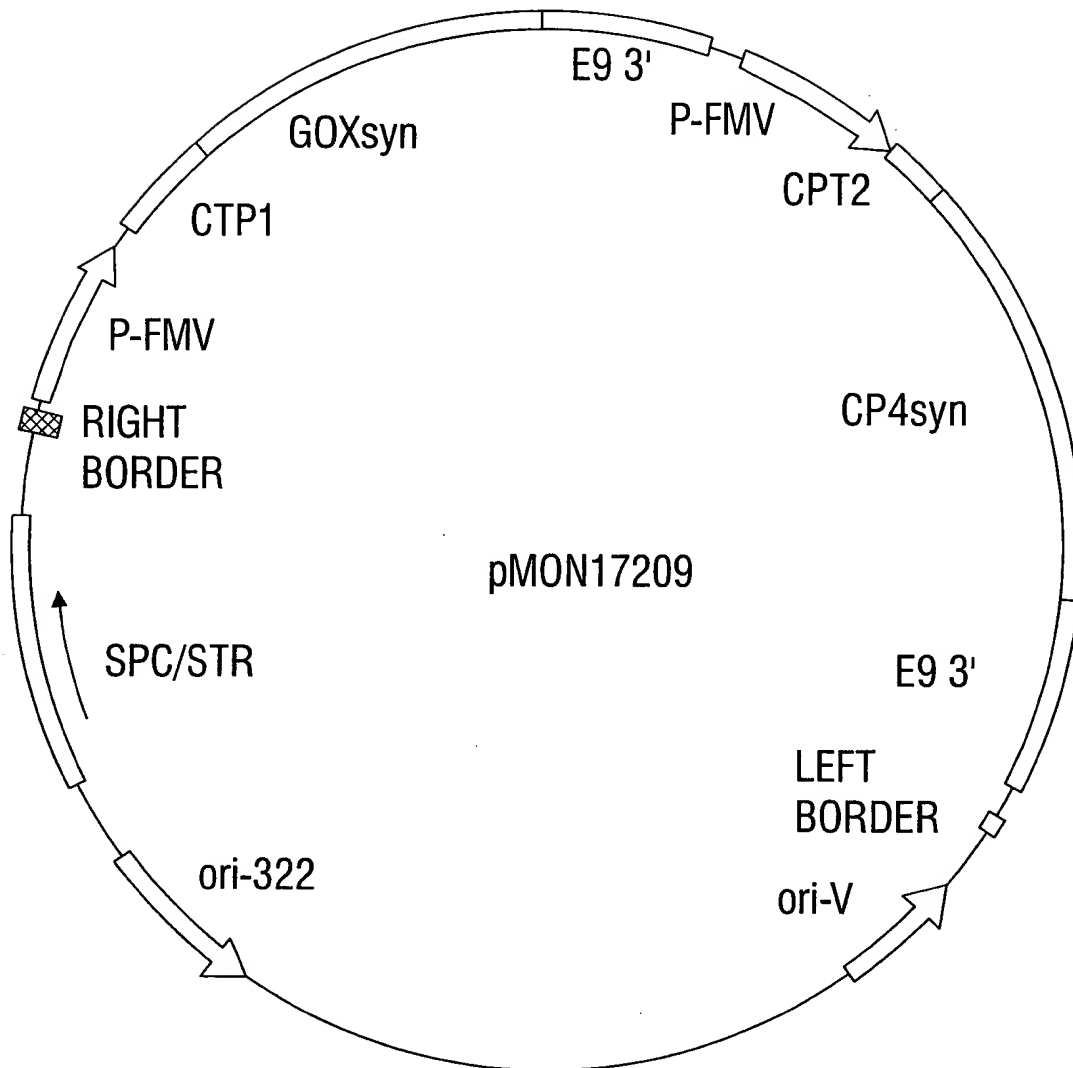


FIG. 24

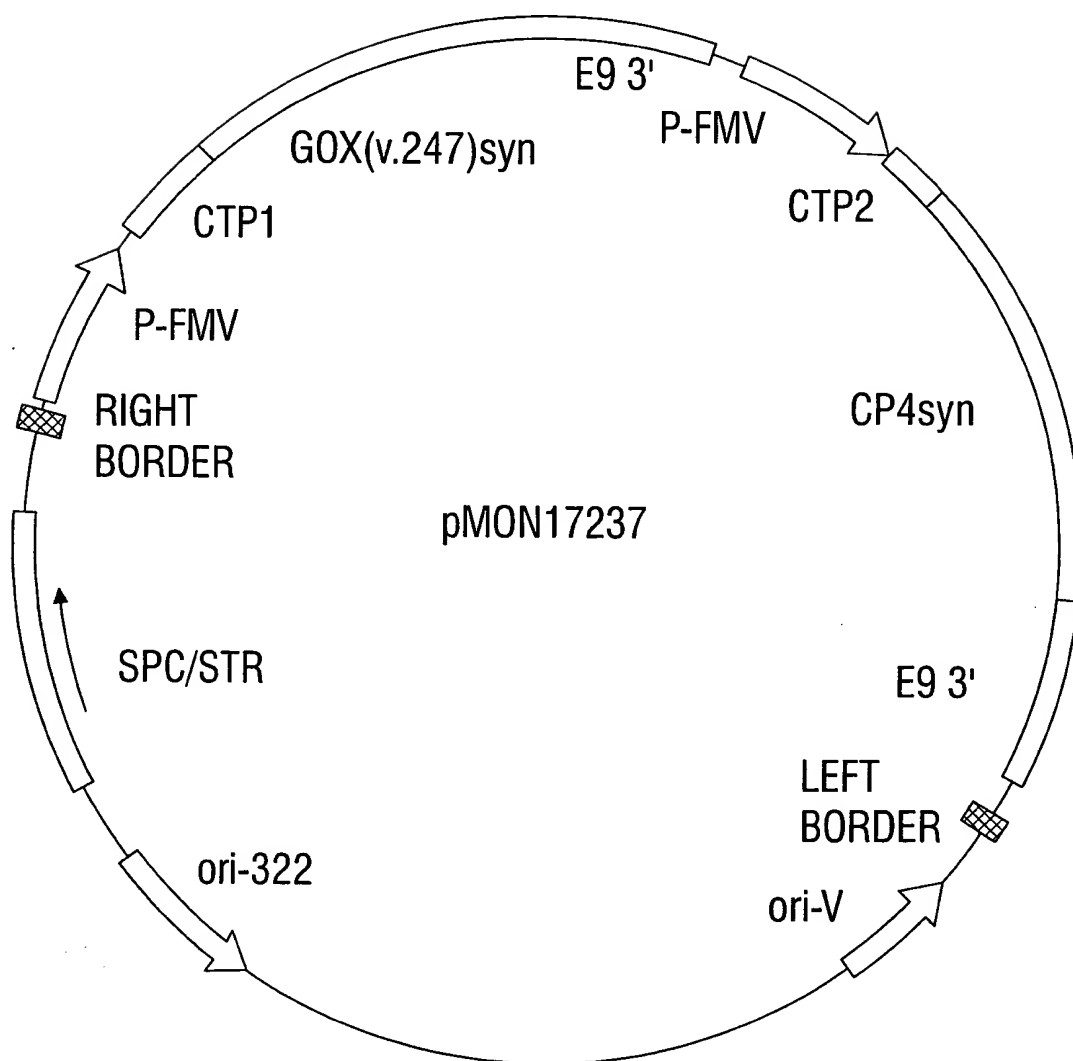


FIG. 25